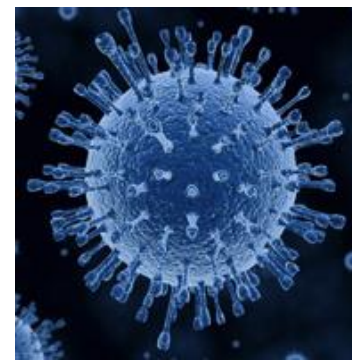
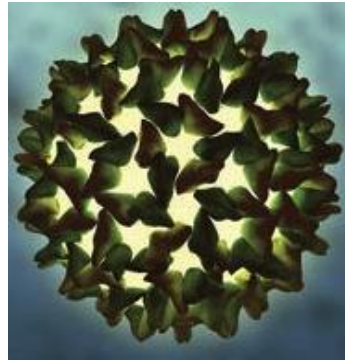
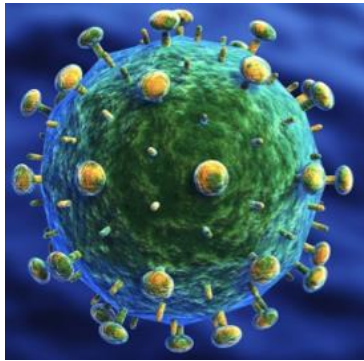


HIV, HBV, HCV

Virology

Anna Maria Geretti
Institute of Infection & Global Health
University of Liverpool

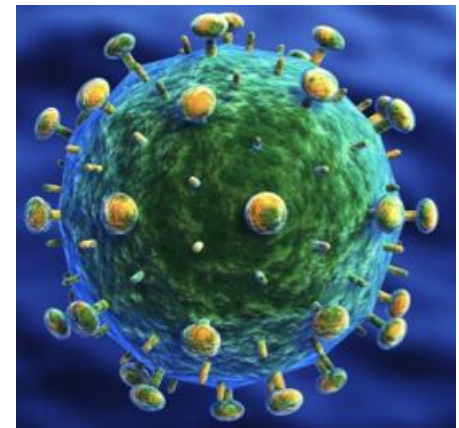


- **Many similarities**
- **Several fundamental differences**

HIV

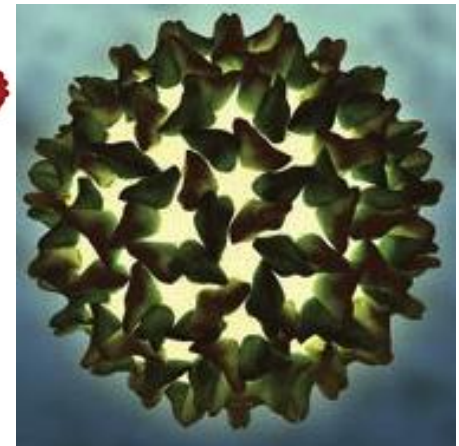
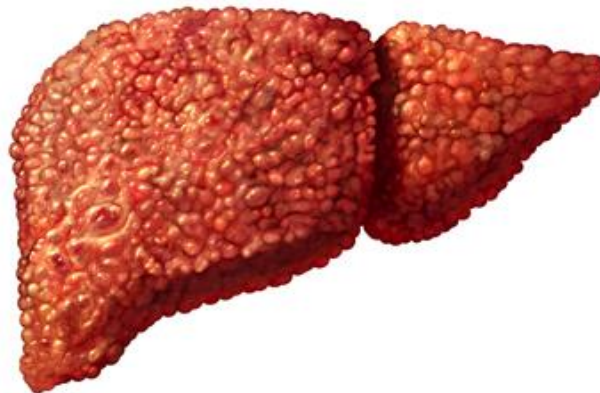
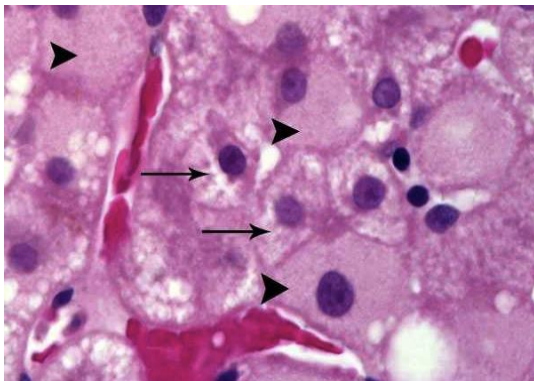
RNA virus

- Chronic infection
- Without treatment, most people develop AIDS and die within ~10 years (7.5 to 11.6)^{1,2}
- Non-AIDS HIV-related disease
- Latent **reservoir** as integrated provirus
- Antiviral therapy **controls** but does not eradicate HIV
- **Life-long** therapy required to suppress virus replication
- **PrEP** and **PEP**



HBV

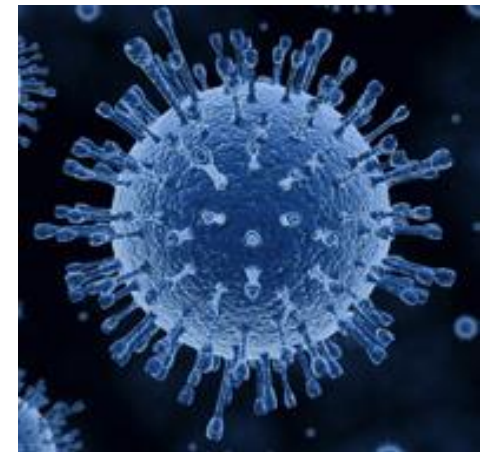
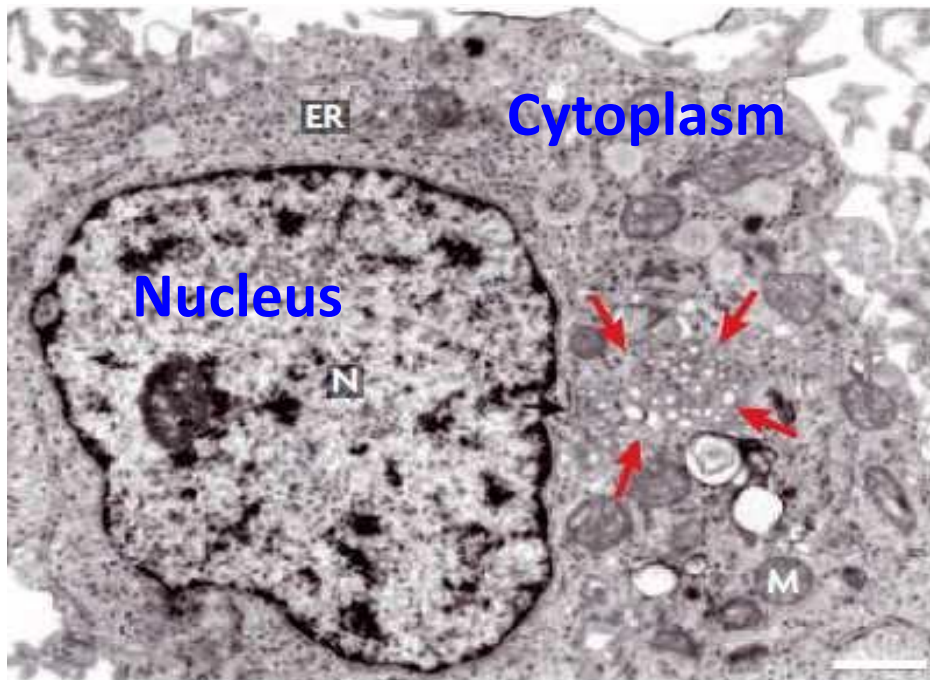
DNA virus	<ul style="list-style-type: none">• Vaccine• Chronic infection in >90% children, <5% adults• Cirrhosis (~30%)• Hepatocellular carcinoma (with/without cirrhosis)• Extra-hepatic disease	<ul style="list-style-type: none">• Persistence as cccDNA, may integrate• Several replicative states• Antiviral therapy not always required, controls but does not eradicate HBV, can be stopped in some cases• Antivirals work as PrEP
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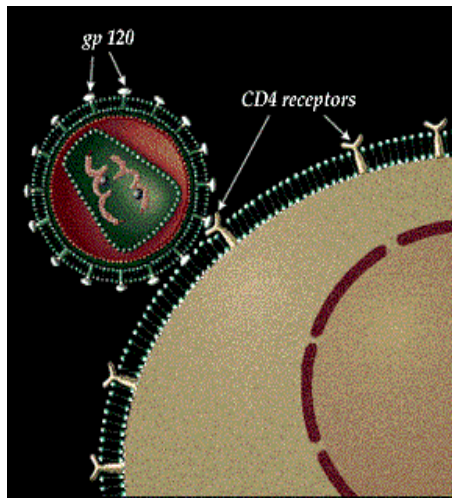


HCV

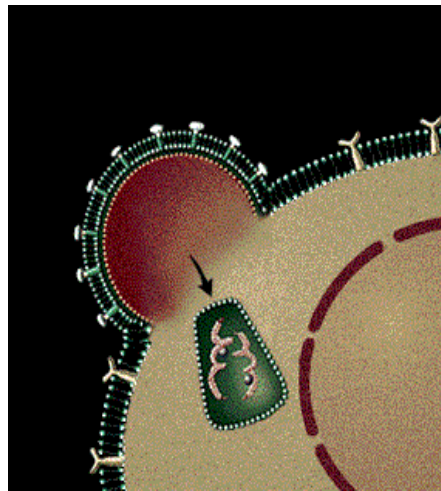
RNA virus

- Chronic infection ~80%
- Cirrhosis (41% over 30 years), hepatocellular carcinoma
- Extra-hepatic disease increasingly recognised^{1,2}
- **No** stable or latent **reservoir**
- **Curable** with antiviral therapy

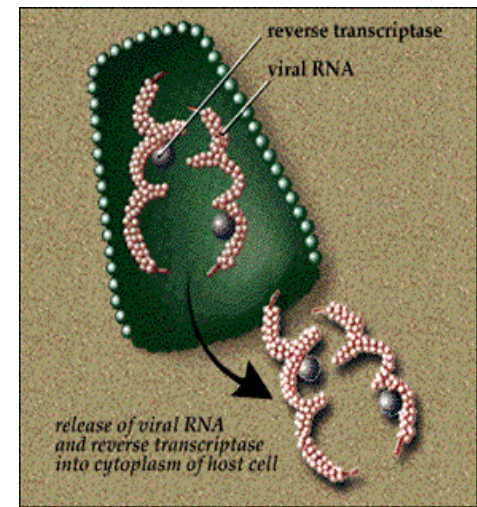




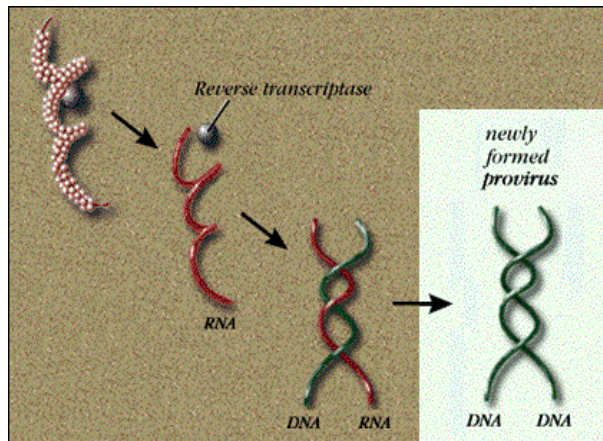
Attachment



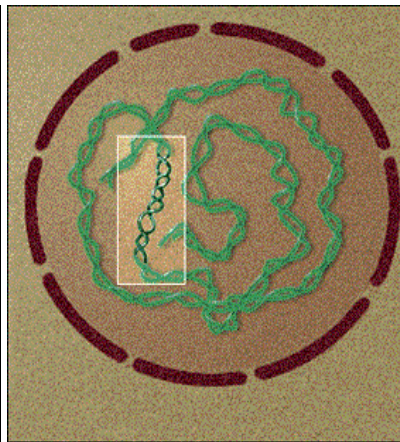
Fusion



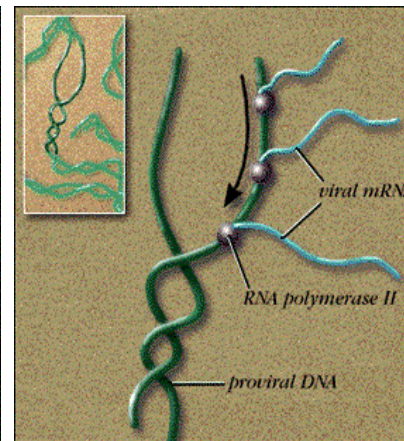
Release of RNA



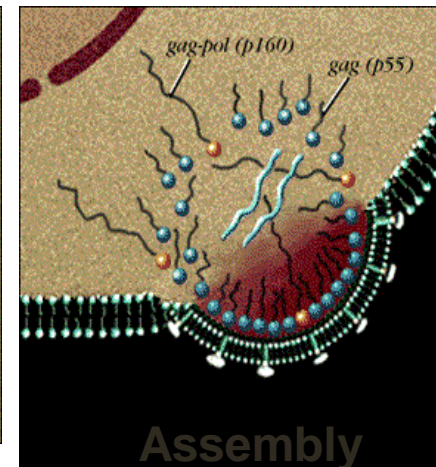
Reverse transcription



Integration



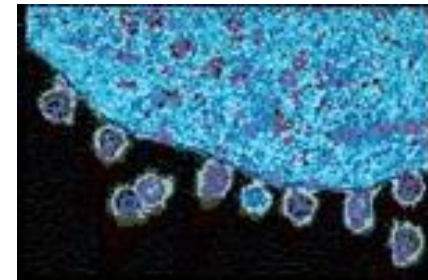
Transcription



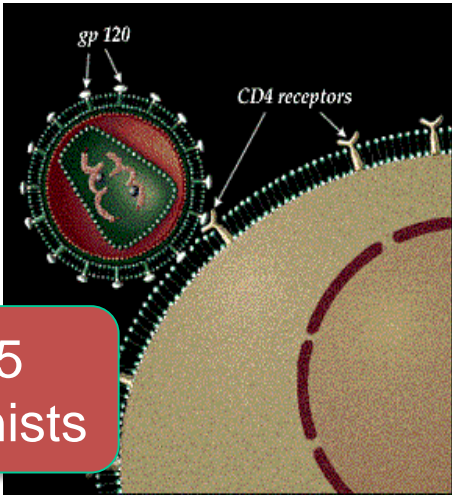
Assembly

HIV replication

**Maturation
& budding**

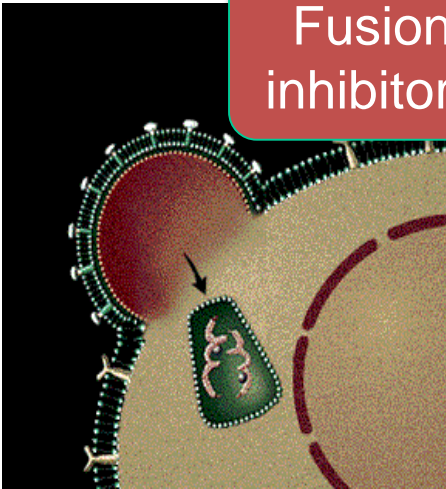


CCR5
antagonists

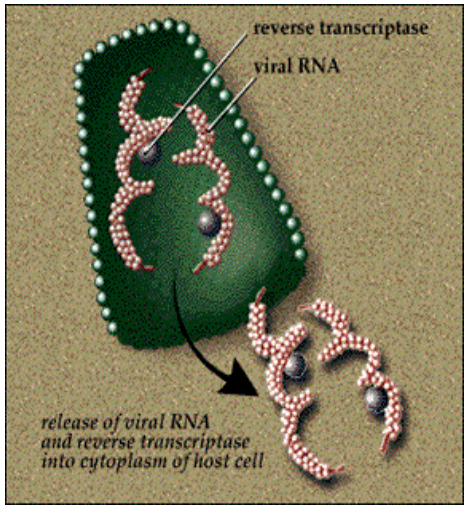


Attachment

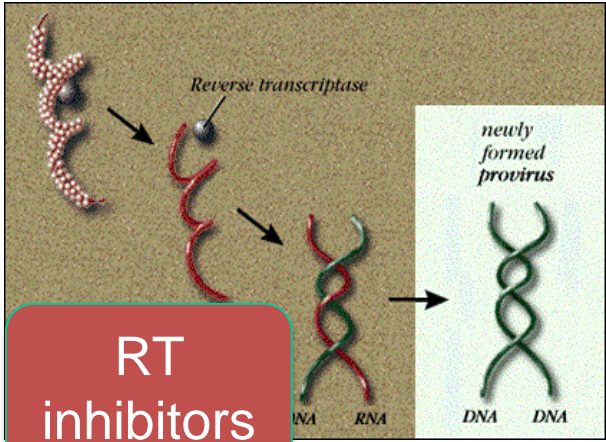
Fusion
inhibitors



Fusion



Release of RNA



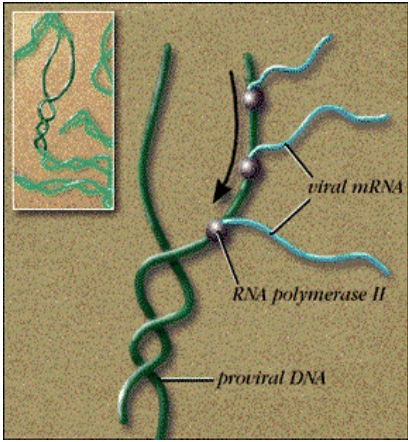
RT
inhibitors

Reverse transcription

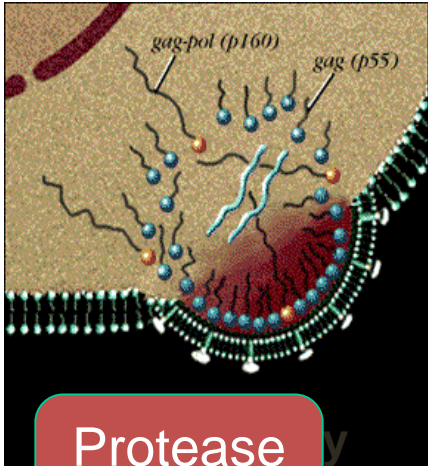


Integrase
inhibitors

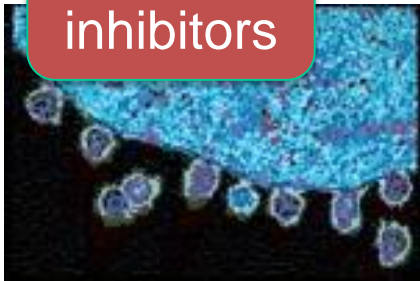
Integration



Transcription



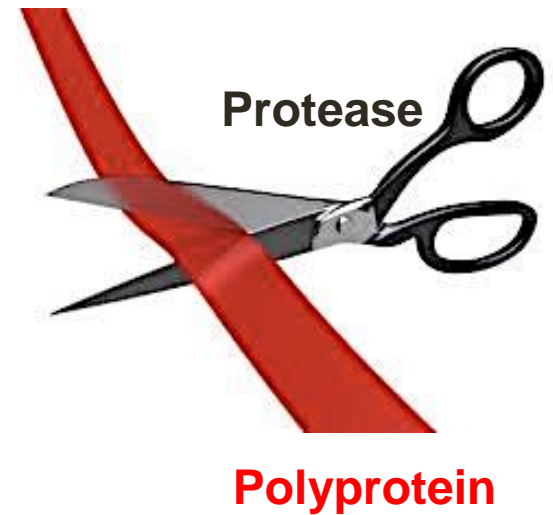
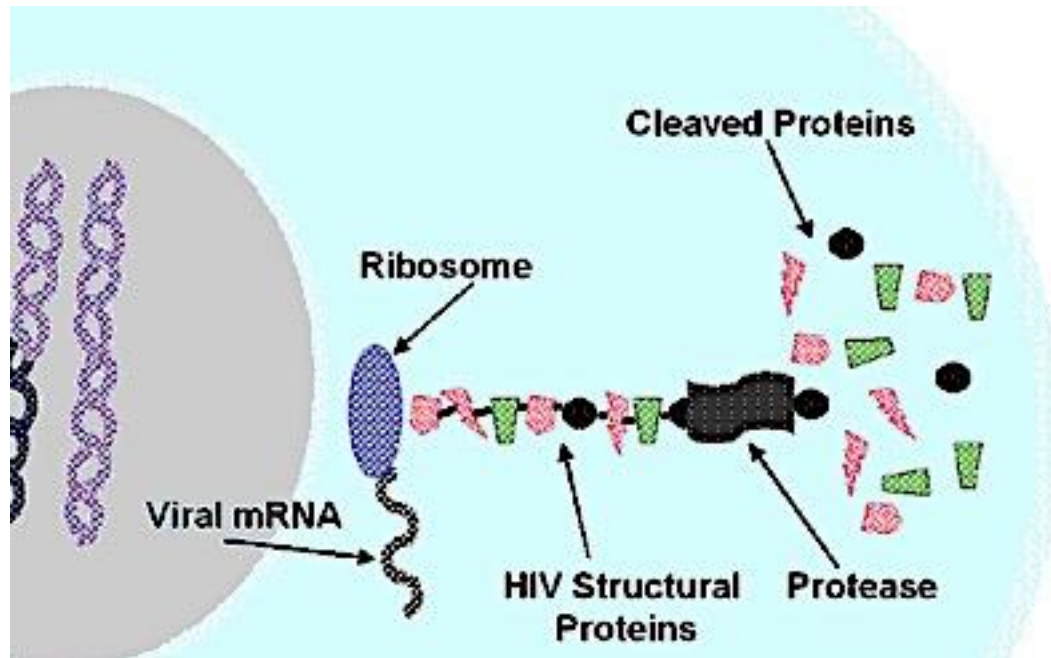
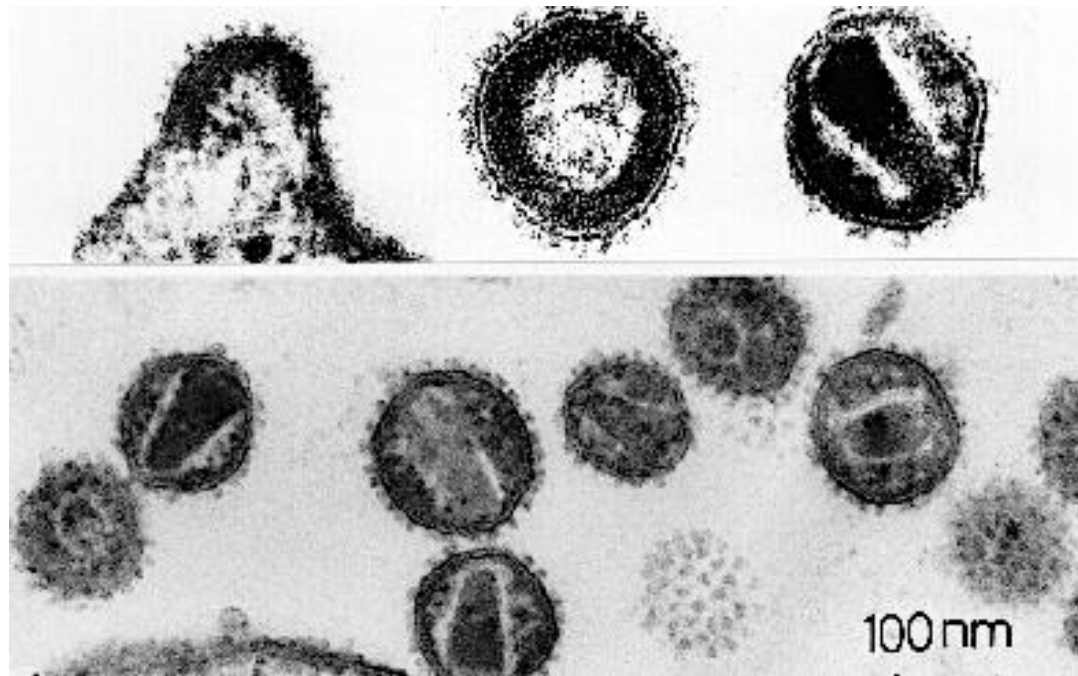
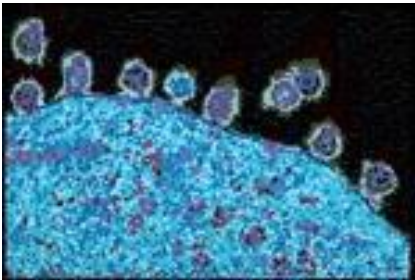
Protease
inhibitors

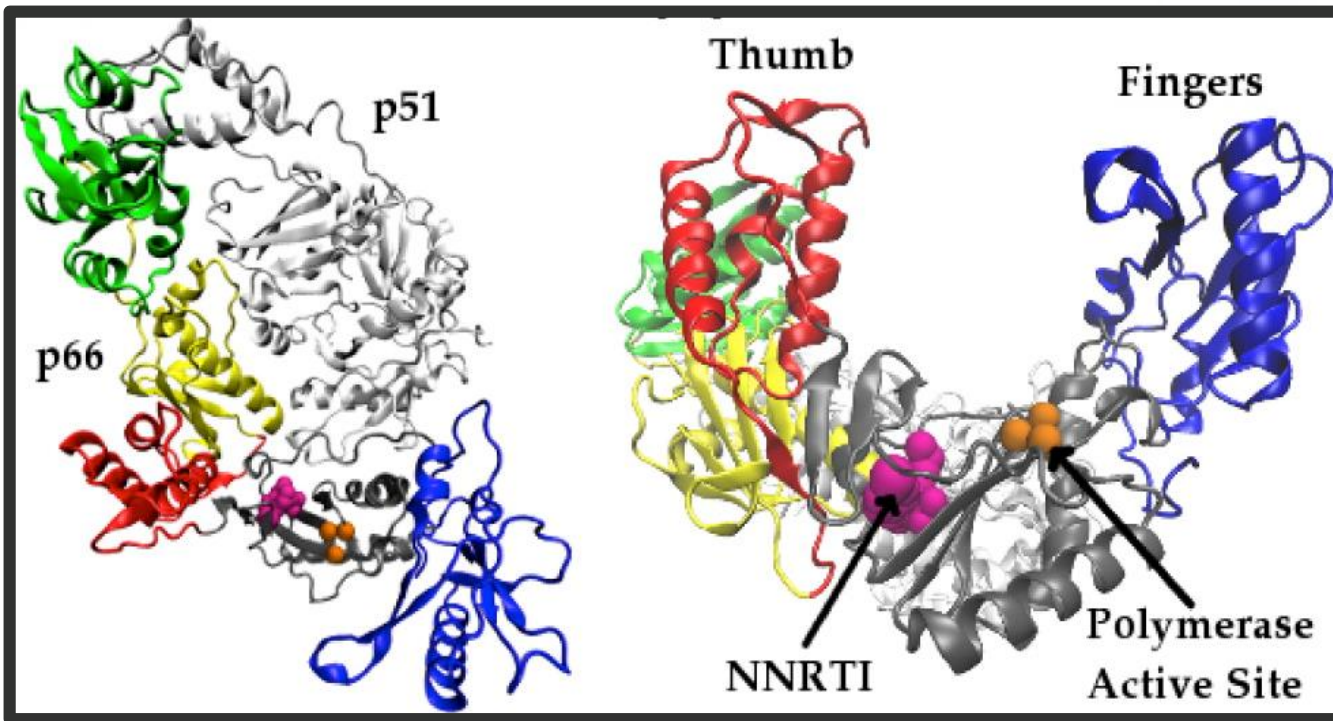


Maturation
& budding

Targets of therapy

Maturation & budding

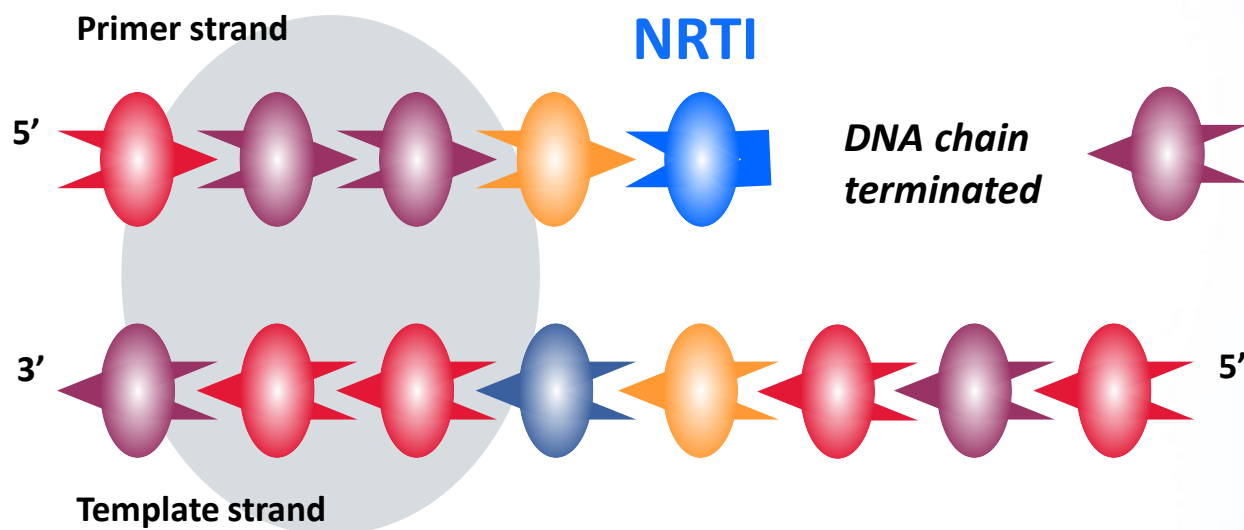
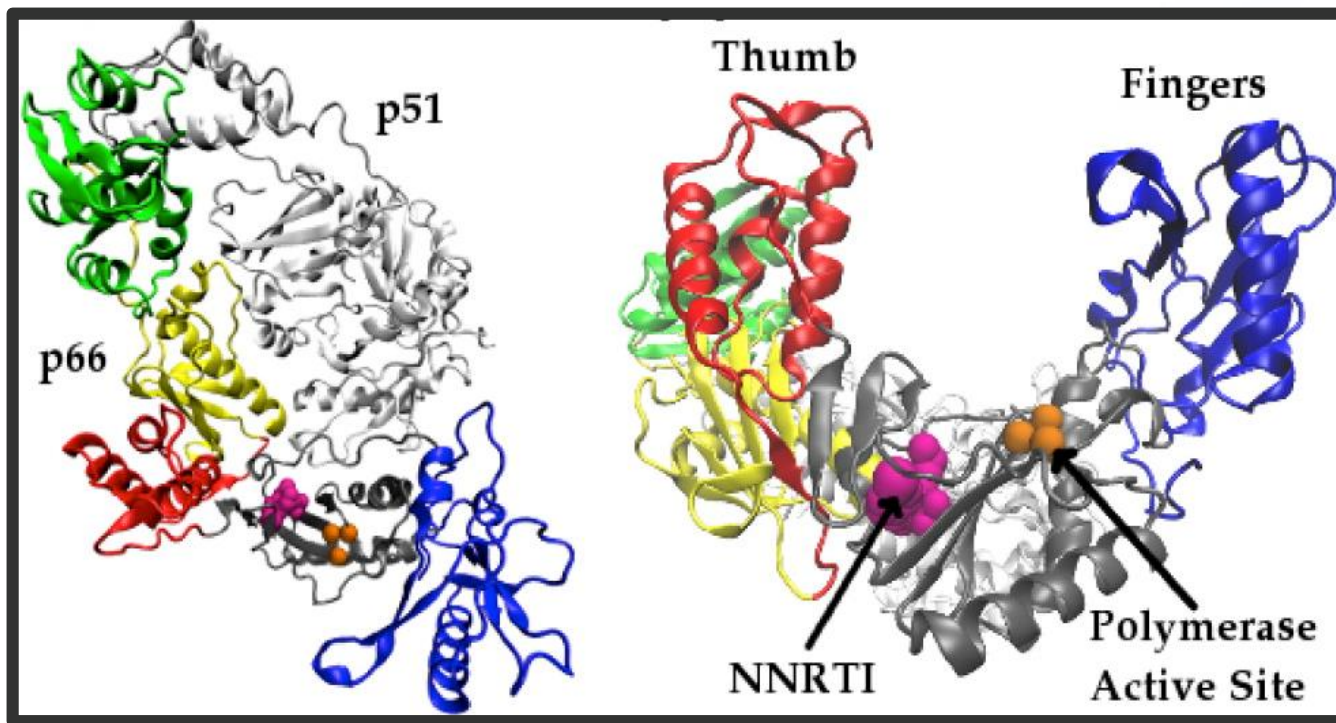




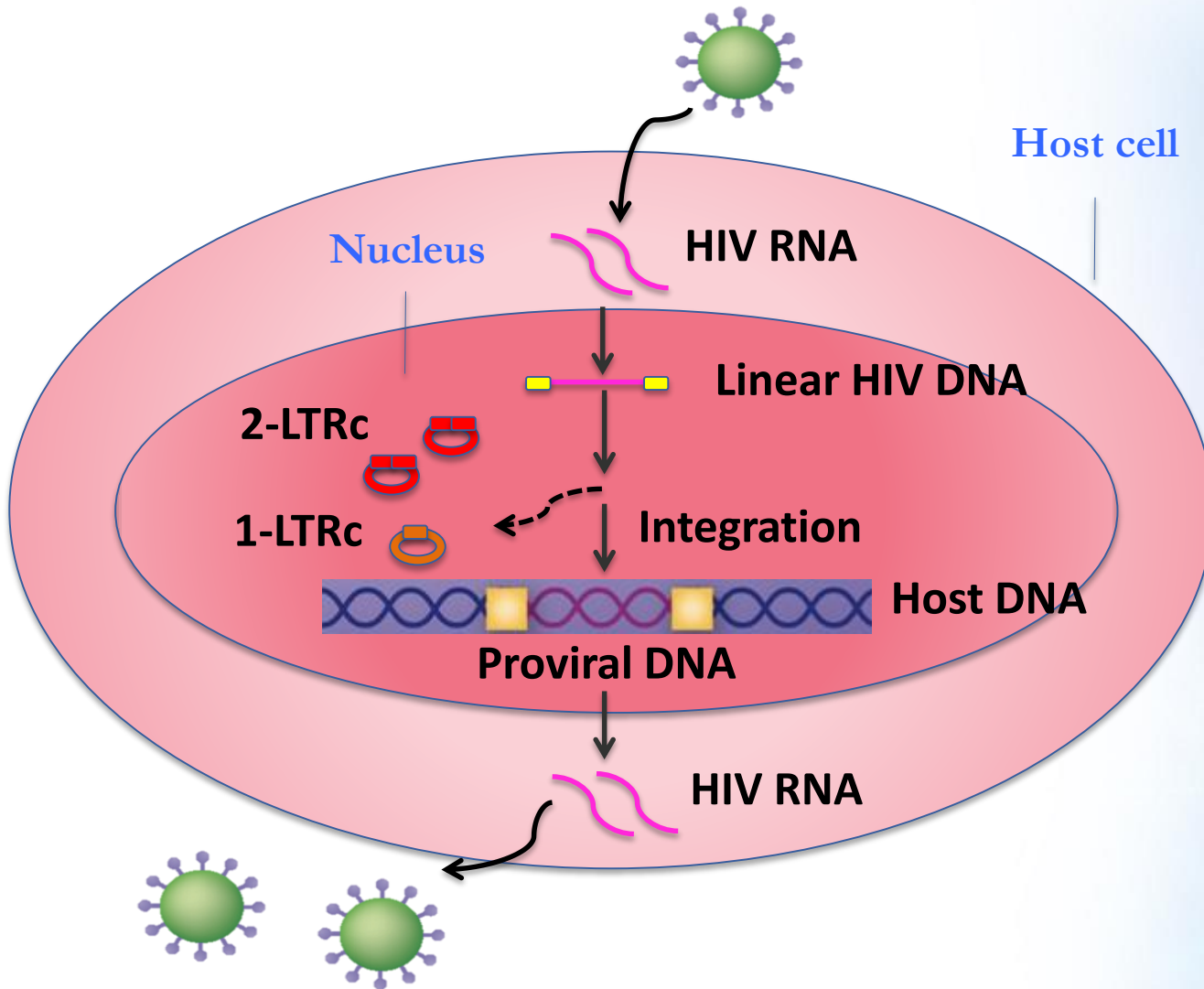
❖ HIV Reverse transcriptase/Polymerase

Two mechanisms of inhibition

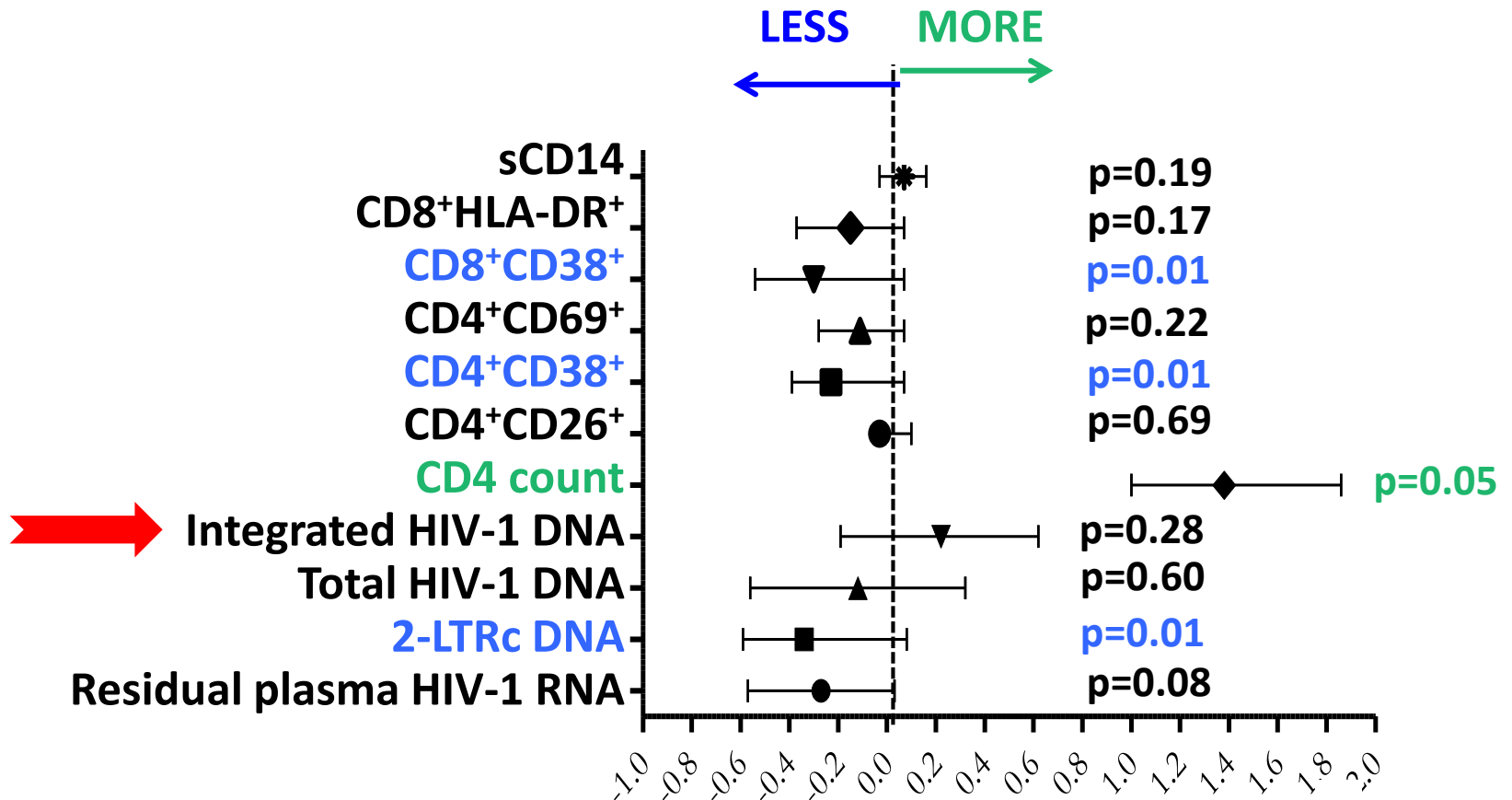
- Competitive – NRTIs
- Allosteric – NNRTIs



HIV DNA forms



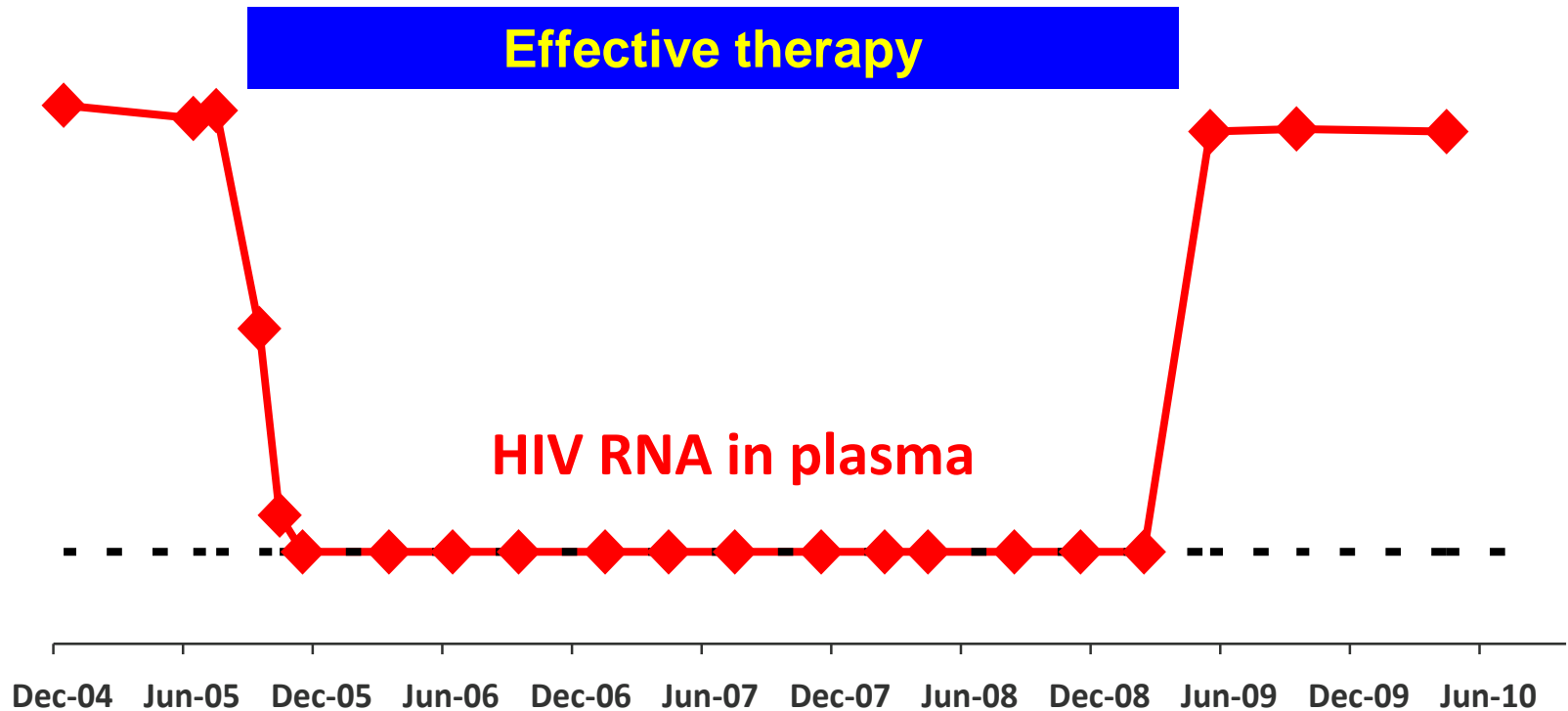
Effect of ART duration on virological & immunological parameters



log-transformed variables

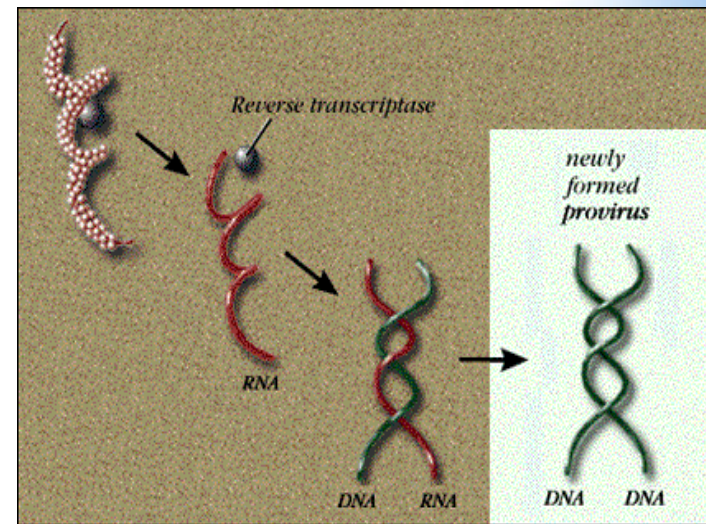
Mean difference per 10 years of suppressive ART

Virus replication resumes if therapy is stopped



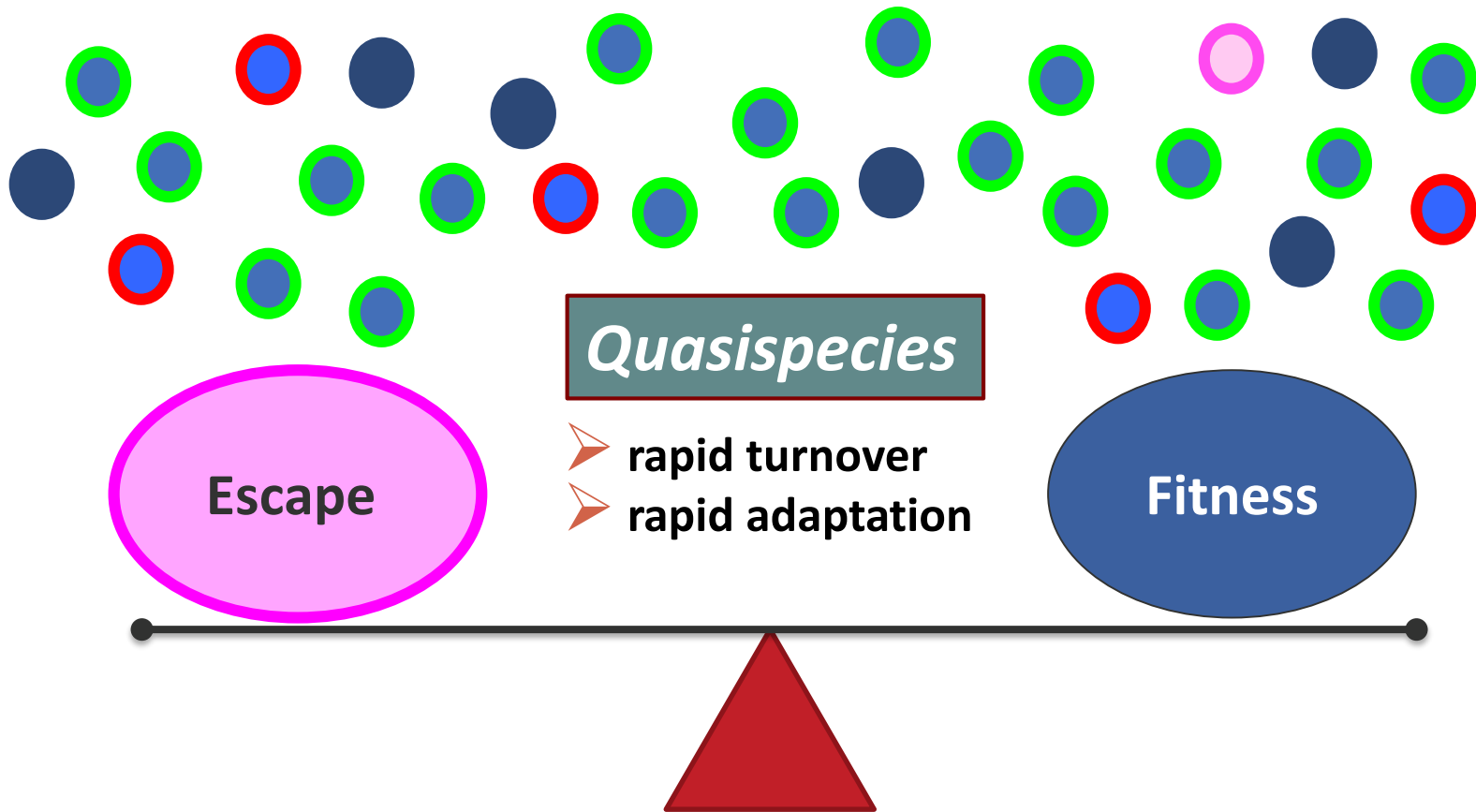
- Antiretroviral therapy cannot achieve HIV eradication
- After stopping therapy HIV replication resumes to pre-treatment levels

Mechanisms of HIV genetic evolution



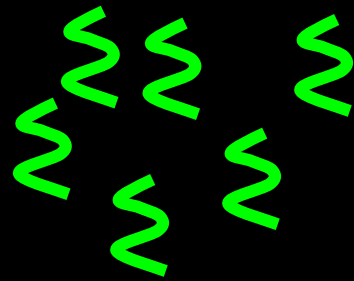
1. Errors by viral reverse transcriptase
 - *~1 mis-incorporation per genome round*
2. Errors by cellular RNA polymerase II
3. APOBEC-driven G→A hypermutation
 - *Deamination of cytosine residues in nascent DNA*
4. Recombination between HIV strains

- Rapid replicating virus ($\sim 10^{10}$ particles/day)
- Rapid clearance of newly produced virus
- Highly error prone polymerase → High mutation rate
- Some mutations detrimental, some allow escape





PCR



Viral gene (e.g., RT)

HIV RNA

Plasma



Sequencing



Mutations

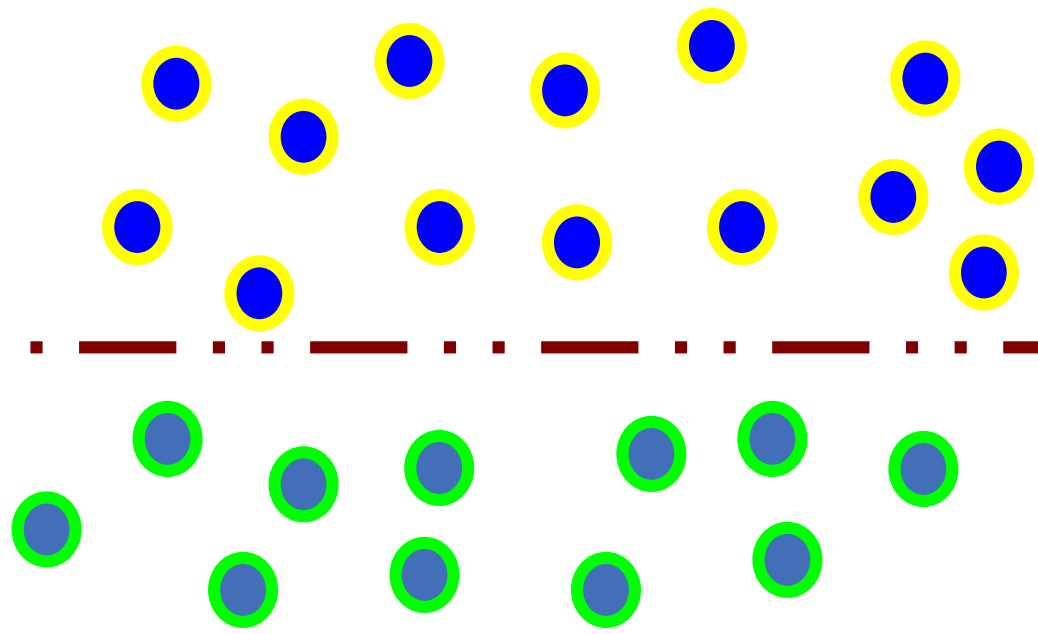
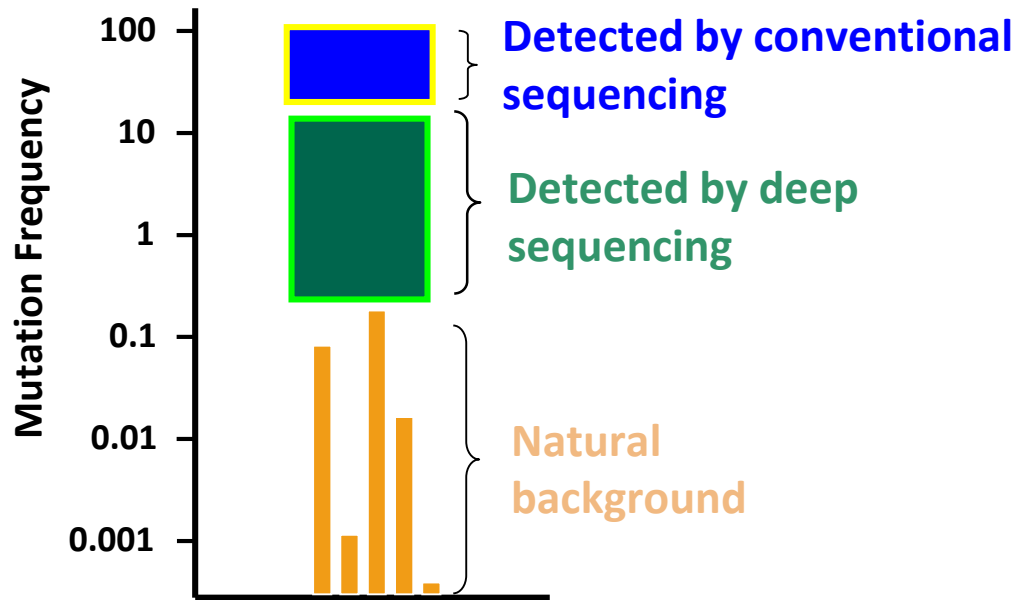
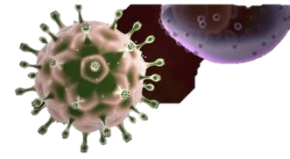


RT **M184V**

Methionine □ **V**aline

@ codon 184 of RT

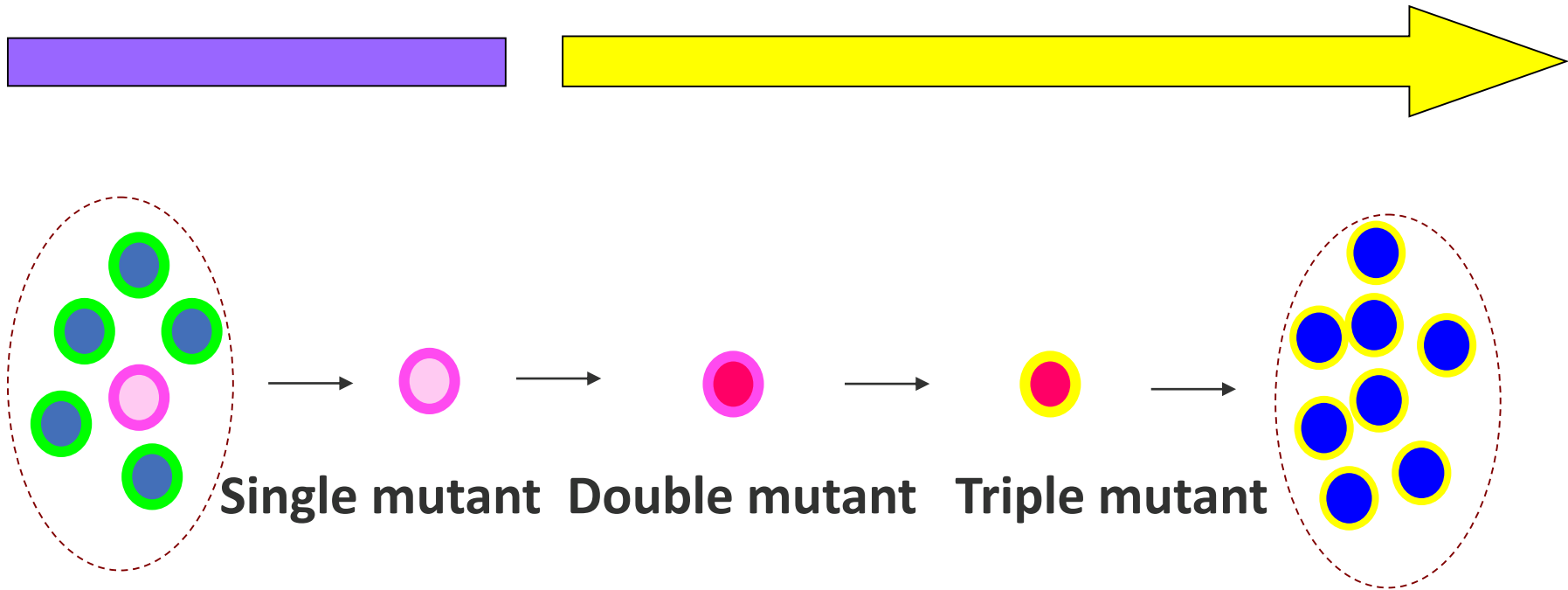
ATG / AUG □ **GTG / GUG**



Limit of detection
of conventional
sequencing

~10-20%

Emergence & evolution of HIV drug resistance



The genetic barrier to resistance is expression of multiple interacting factors

- Virus sequence
- Phenotypic effect of individual mutations
- No. of mutations required to reduce drug susceptibility
- Fitness cost of the mutation
- Ease of emergence of compensatory adjustments

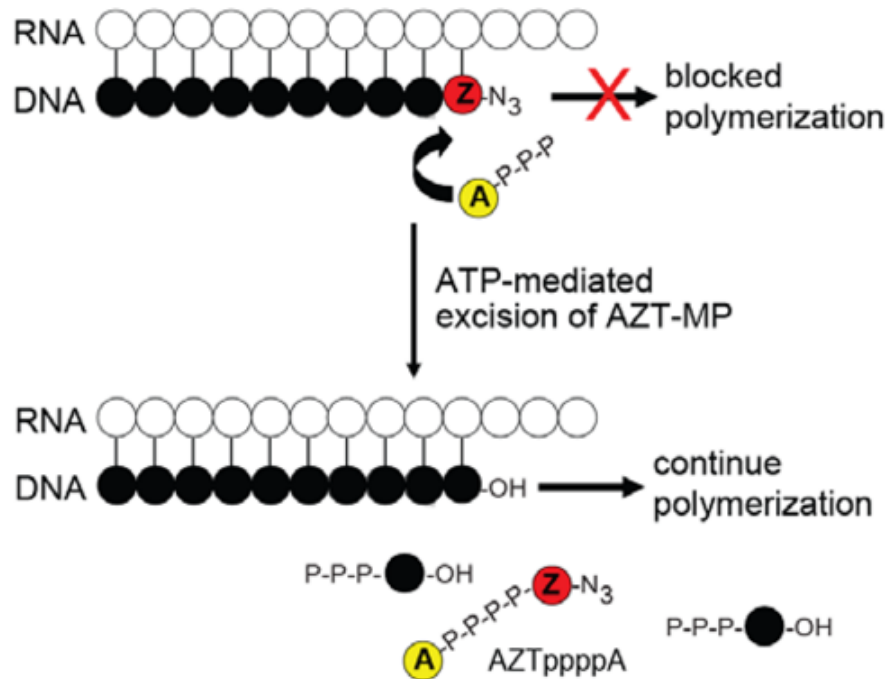
- Drug potency
- Mode of interaction between drug and target
- Drug concentration
- Drug combination
- Antagonism or synergism between resistance pathways

- Viral load
- Host genetics
- Host immune function
- Reservoirs of replications

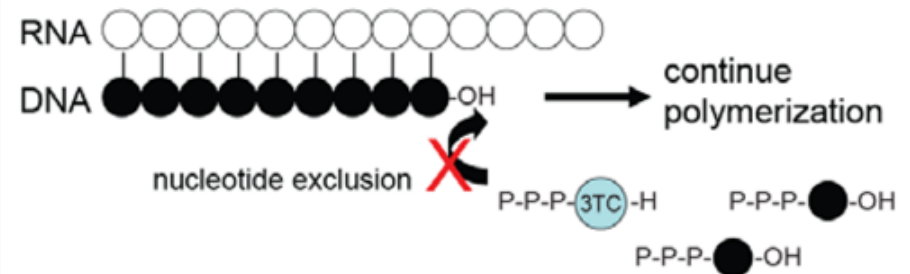
More than the sum of each drug in a regimen

Mechanisms of NRTI resistance

(A) NUCLEOTIDE EXCISION



(B) NUCLEOTIDE DISCRIMINATION

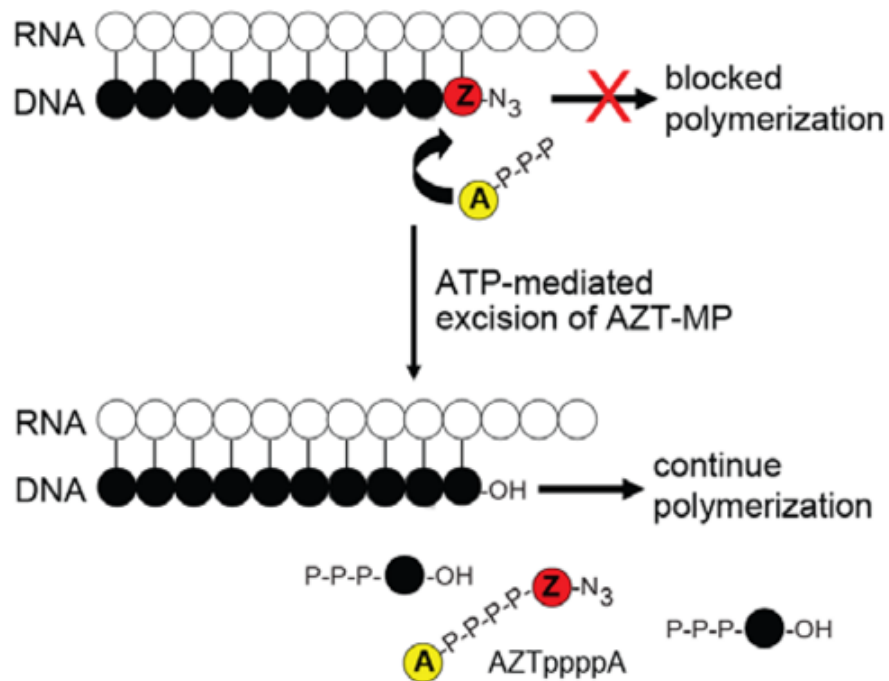


- **M184V (3TC, FTC)**

- **T215Y (AZT, ABC, ddi, d4T, TDF)**

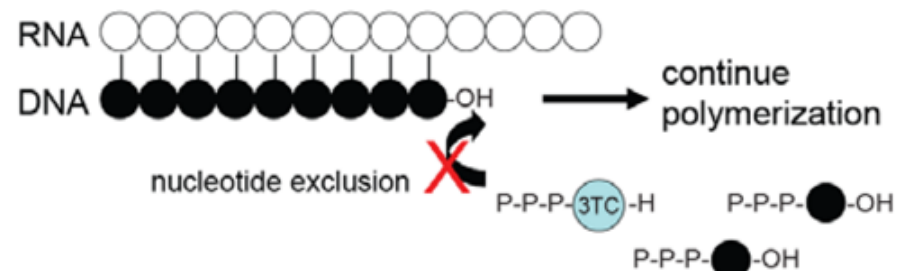
Mechanisms of NRTI resistance

(A) NUCLEOTIDE EXCISION



■ T215Y

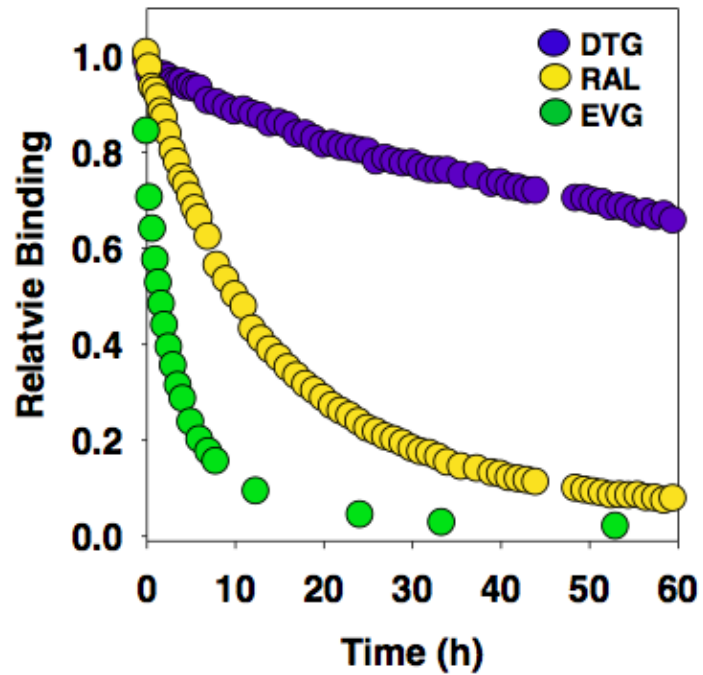
(B) NUCLEOTIDE DISCRIMINATION



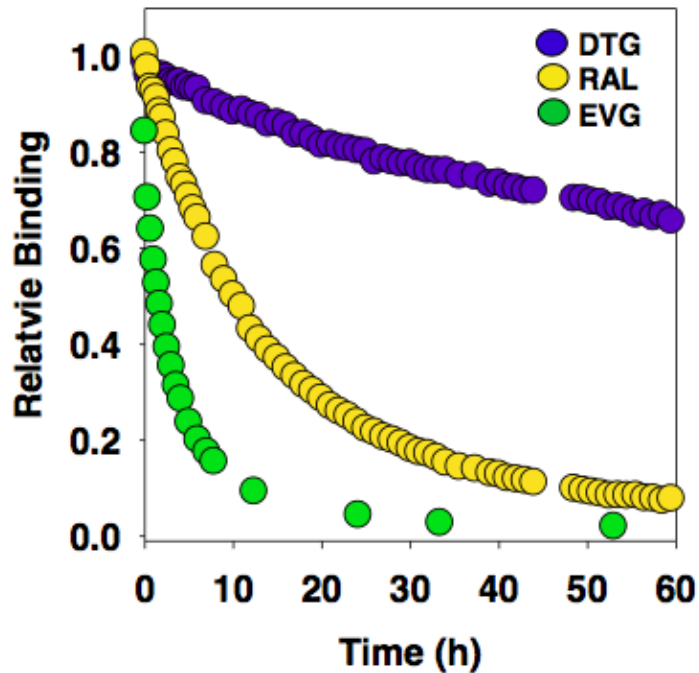
■ M184V

Antagonised by M184V

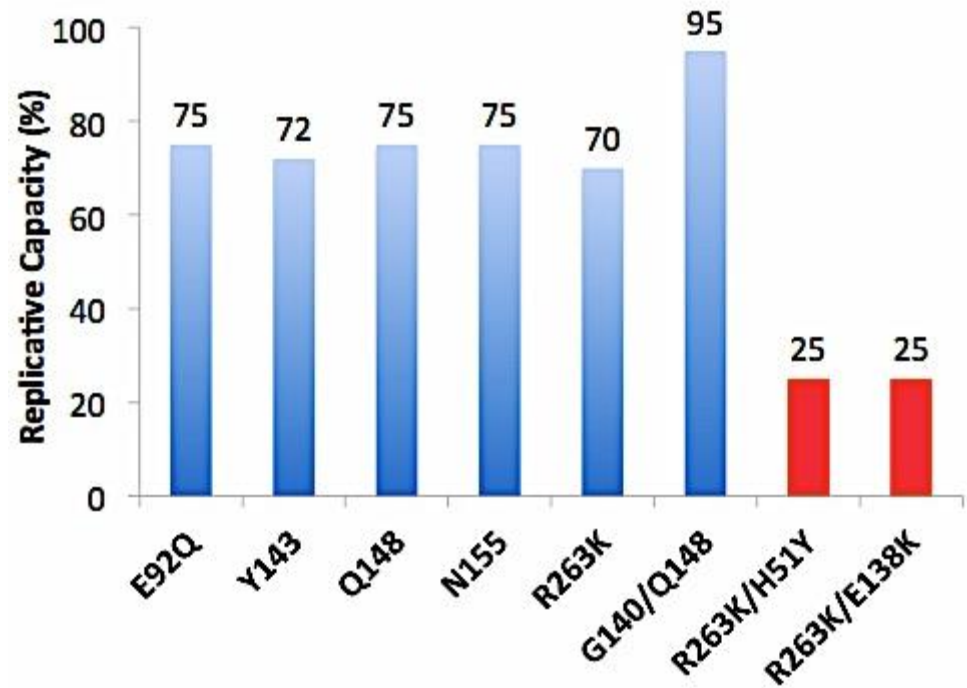
Dissociation time of integrase inhibitors



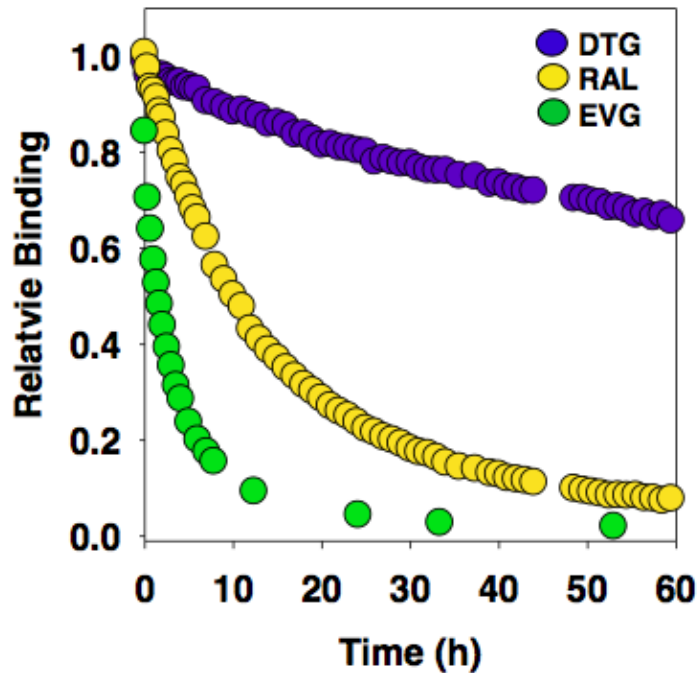
Dissociation time of integrase inhibitors



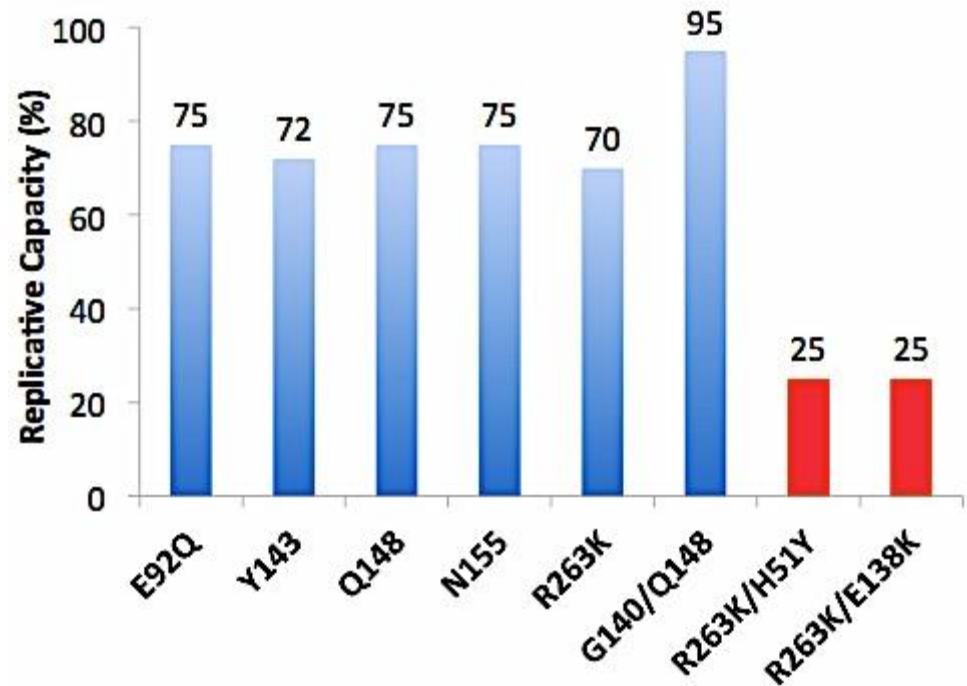
Replicative capacity of integrase mutants



Dissociation time of integrase inhibitors



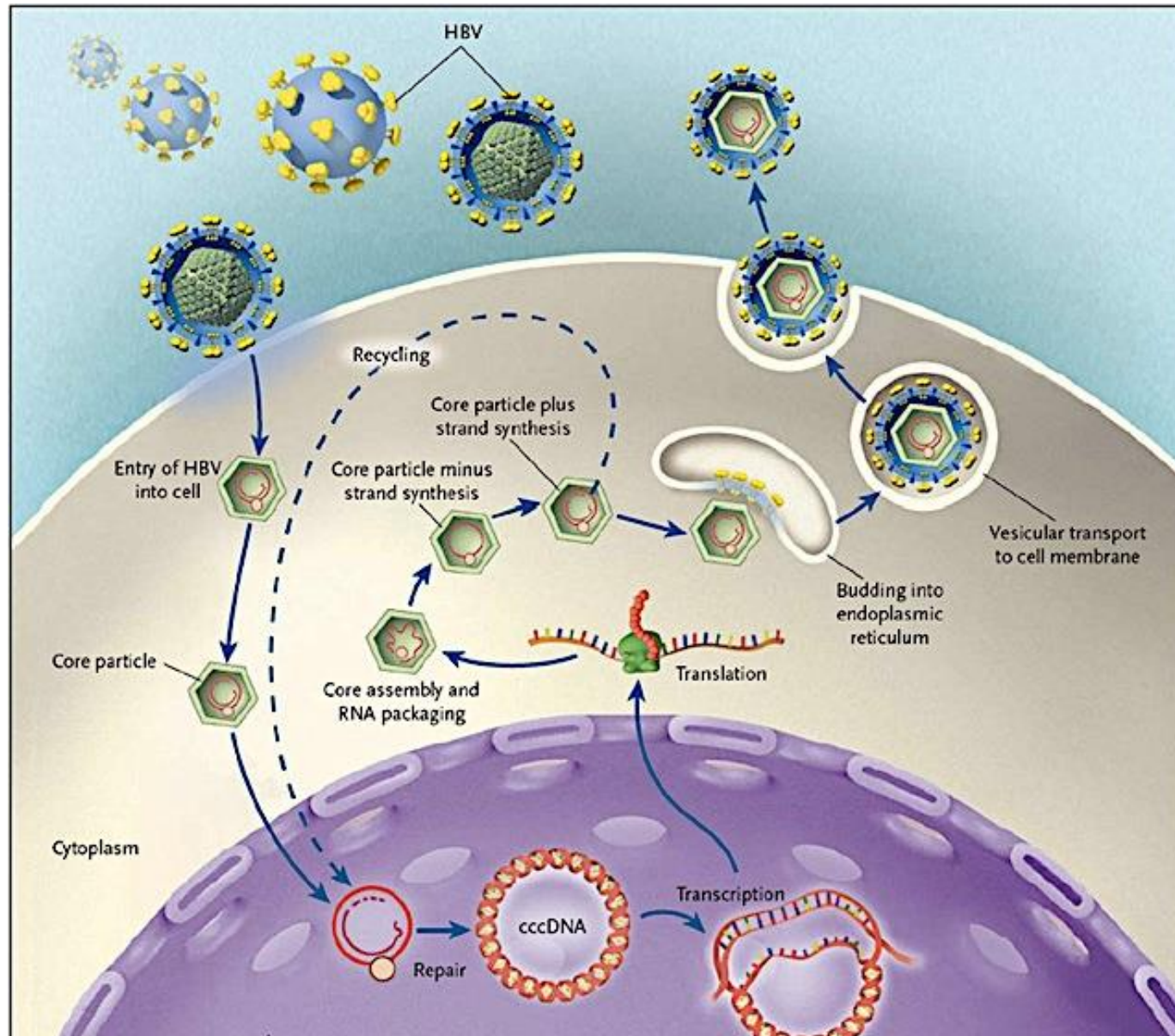
Replicative capacity of integrase mutants



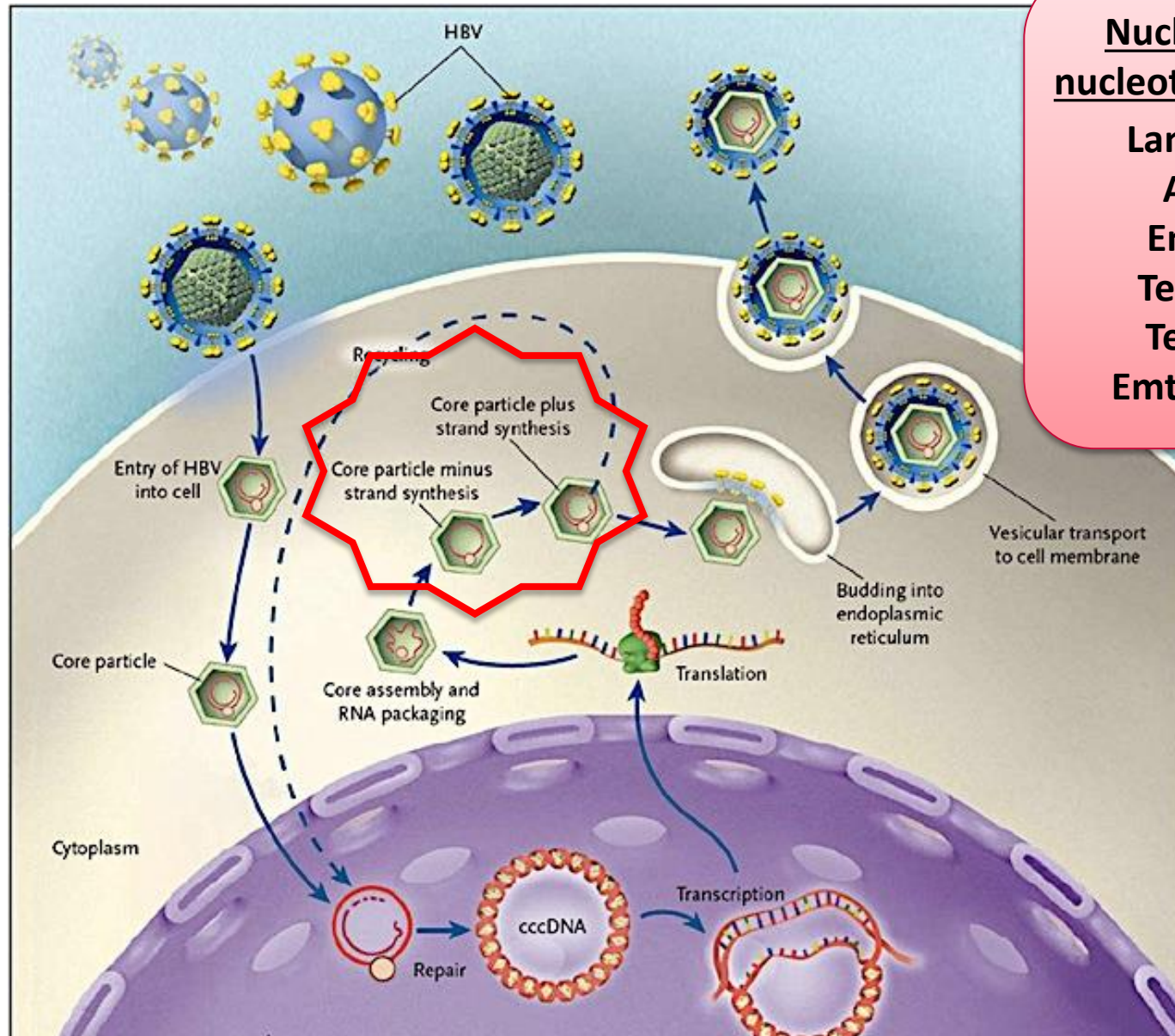
GGT or GGC → Glycine ← **GGA or GGG**
 subtype B AGT or AGC non-B subtypes
 Serine

Codon usage at integrase position 140 in B vs. non-B subtypes

HBV replication



HBV drug targets



Nucleoside and nucleotide analogues

Lamivudine*

Adefovir

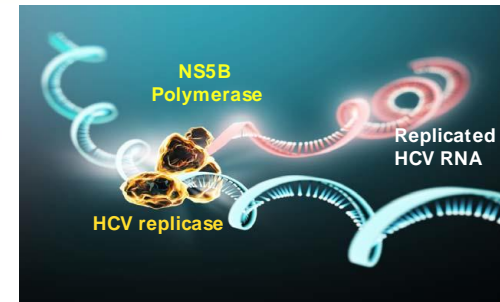
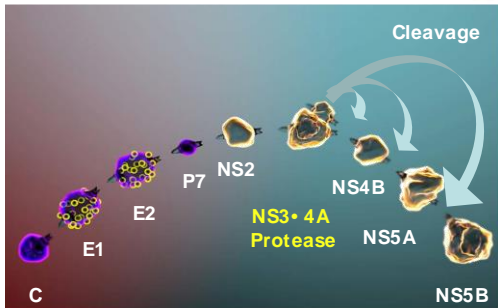
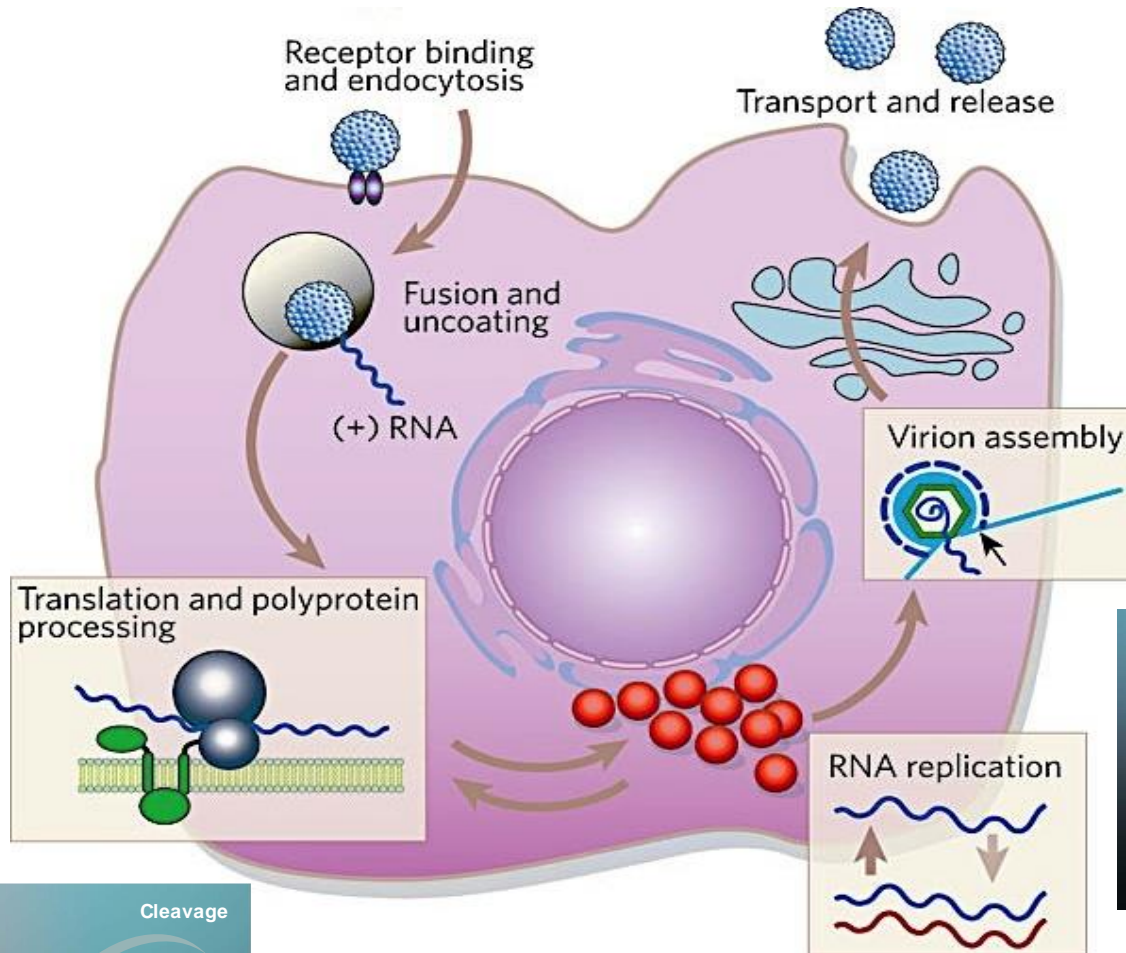
Entecavir*

Telbivudine

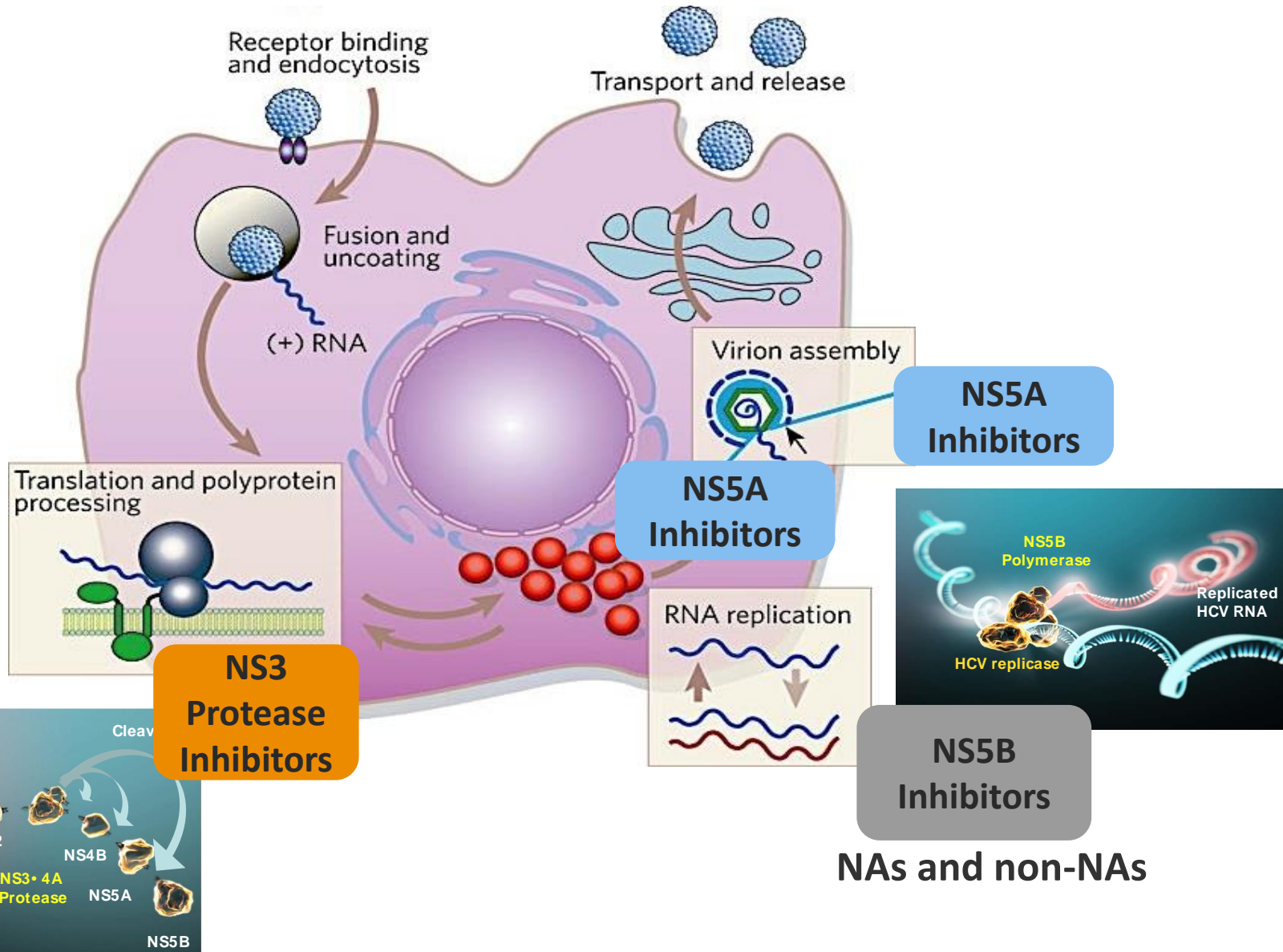
Tenofovir*

Emtricitabine*

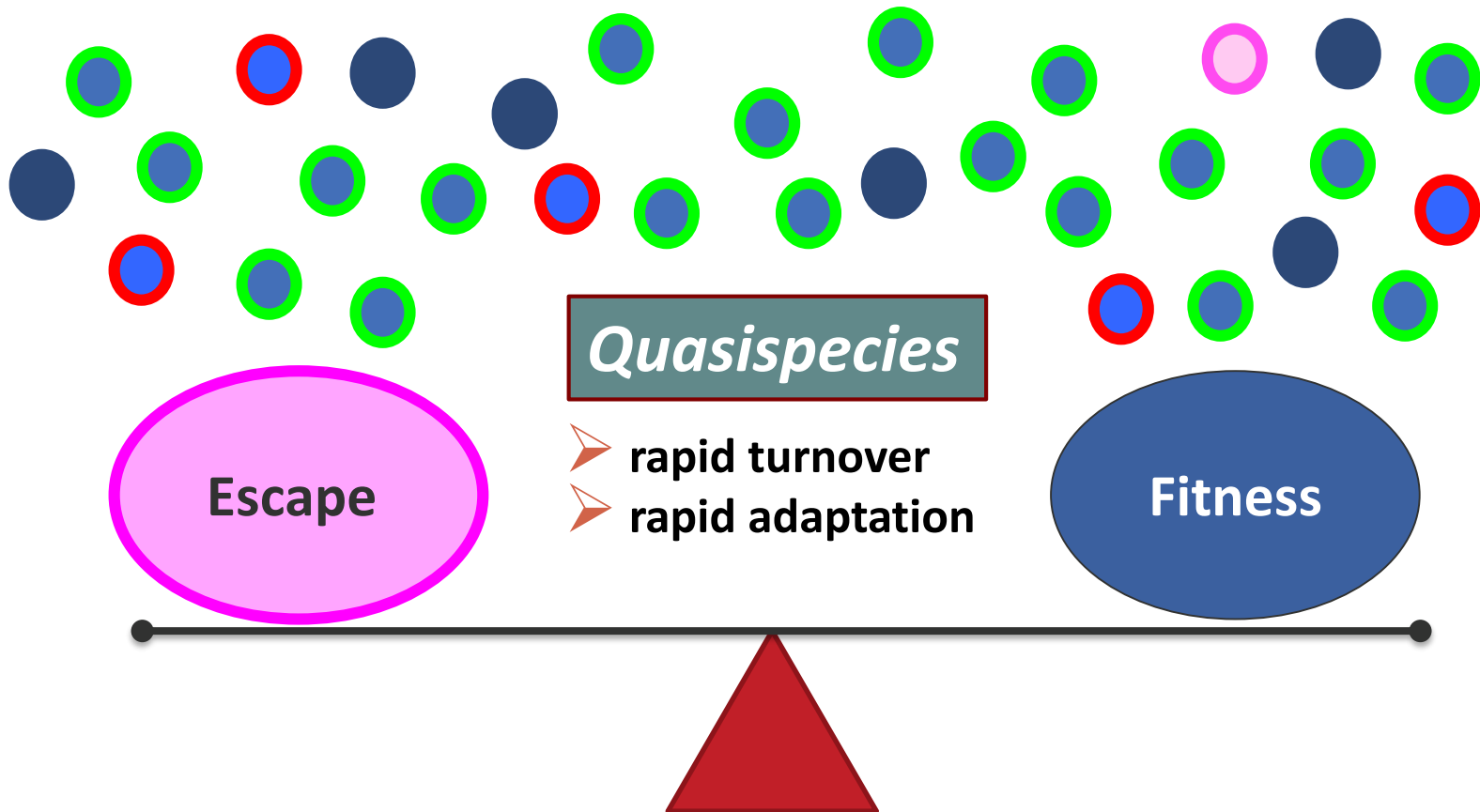
HCV replication

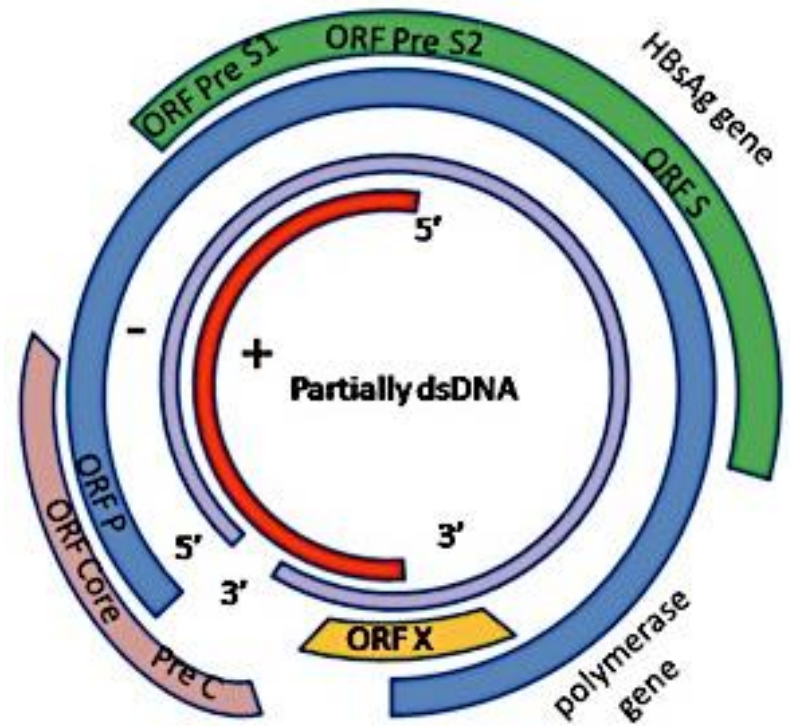
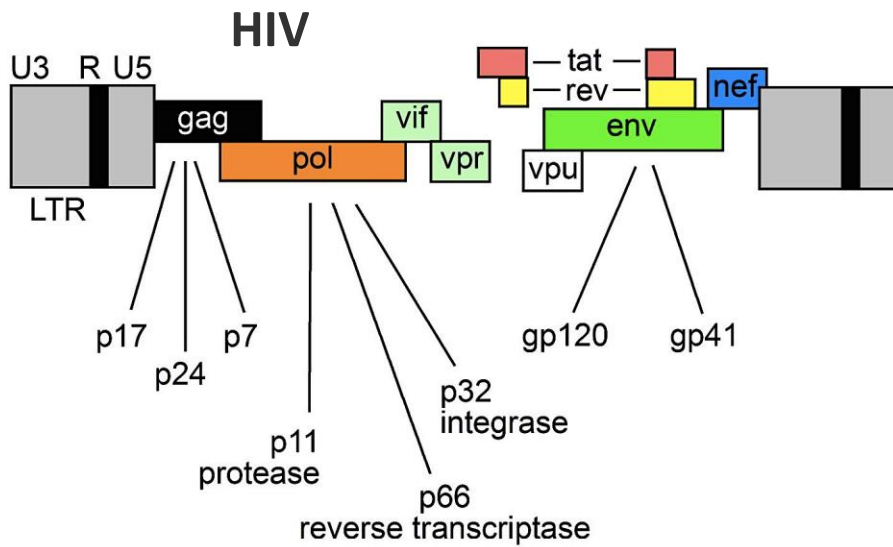


HCV drug targets



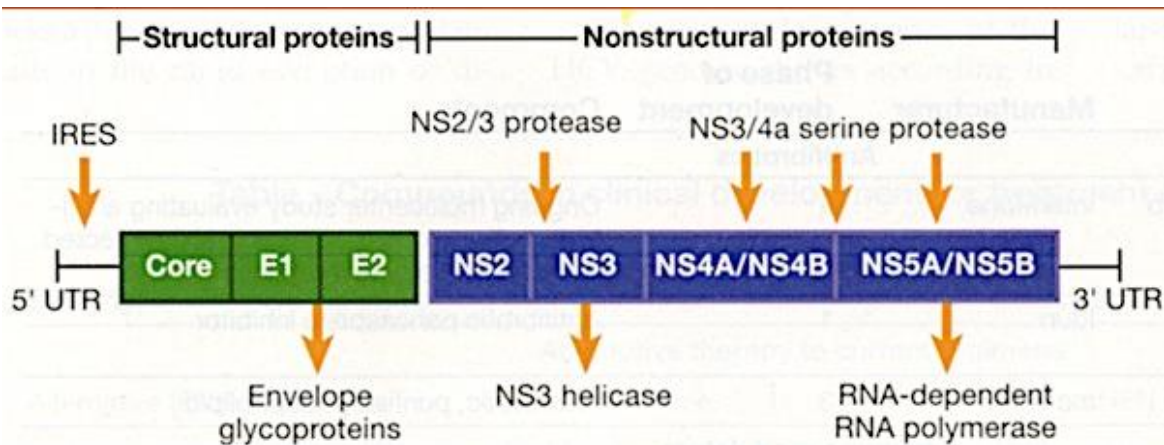
- Rapid replicating virus (HIV 10^{10} - **HBV 10^{11} - HCV 10^{12} particles/day**)
- Rapid clearance of newly produced virus
- Highly error prone polymerase → High mutation rate
- Some mutations are detrimental, some allow escape





HBV

HCV



Incidence of HBV drug resistance

Years 1-5; first-line therapy

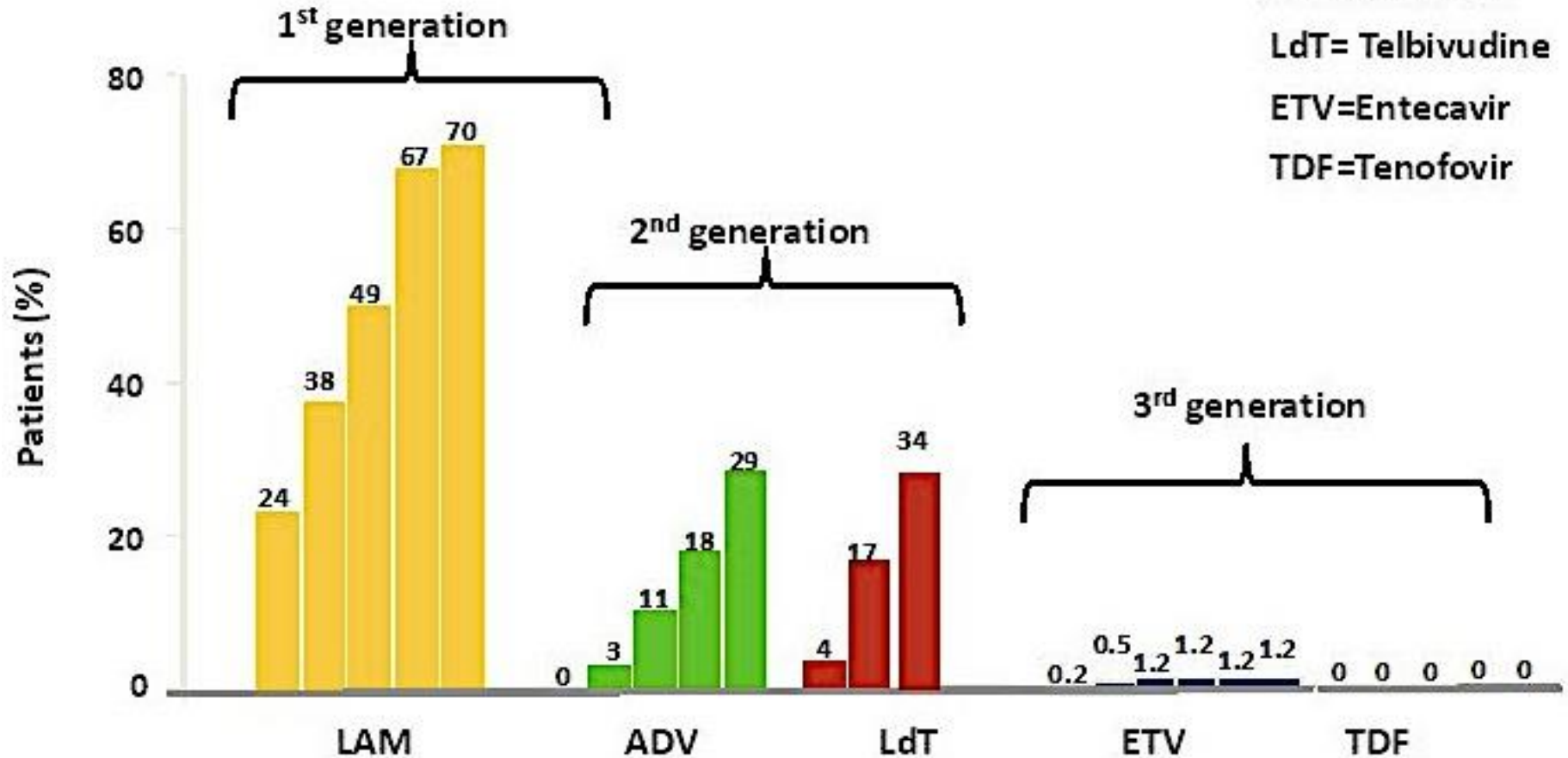
LAM= Lamivudine

ADV=Adefovir

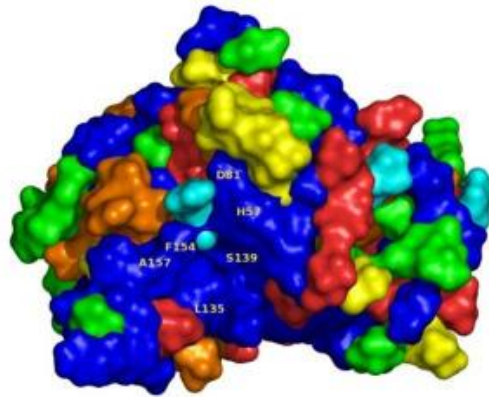
LdT= Telbivudine

ETV=Entecavir

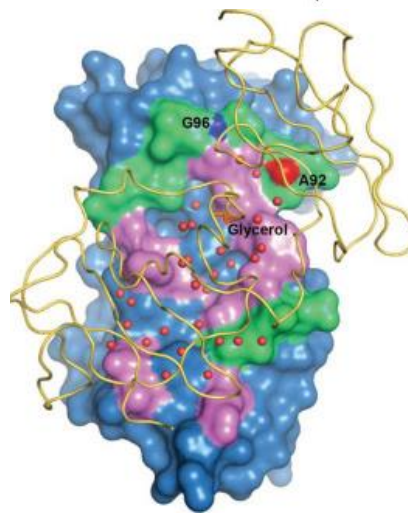
TDF=Tenofovir



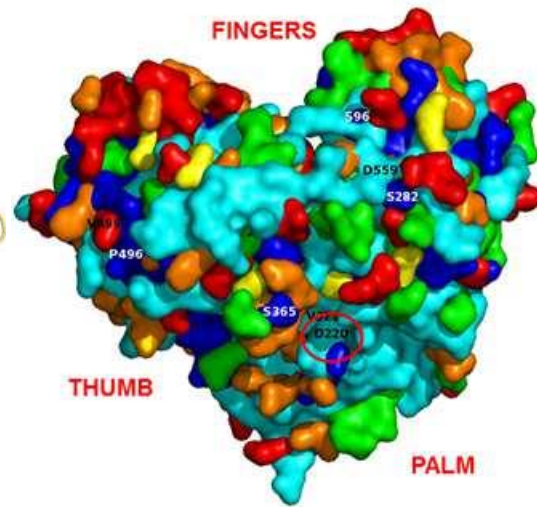
HCV genetic variability



NS3: 42% of amino acid conserved among all genotypes



NS5A: 46% of amino acid conserved among all genotypes



NS5B: 55% of amino acid conserved among all genotypes

Prevalence of NS3 resistance mutations in naïve patients with HCV Gt1a

RAMs	CS & DS	DS
	>10%	1-10%
	n(%)	n(%)
36M	1(0.4)	2(1.1)
36L	5(2.1)	0(0)
54S	9(3.8)	0(0)
55A	10(4.2)	0(0)
80K	14(18.5)	0(0)
168E	1(0.4)	0(0)
170A	1(0.4)	0(0)
170T	0(0)	2(1.1)

RAMs = Resistance-associated mutations

- HCV treatment-naïve subjects
- Tested by Conventional Sequencing (CS) and Deep Sequencing (DS, Illumina)
- Most mutations detected by CS (= dominant)
- No difference in HCV RNA load in samples with vs. without resistance (= preserved fitness)

Profile of HCV treatment options

	<u>TARGET of THERAPY</u>				
	Protease 1 st gen	Protease 2 nd gen	NS5A	NS5B NAs	NS5B non-NAs
Resistance profile	■	■	■	■	■
Genotype coverage	■	■	■	■	■
Potency	■	■	■	■	■

■ Least favourable profile

■ Average profile

■ Good profile

Key points:

Drug resistance with HIV, HBV, HCV

- ❖ Drug-resistant mutants emerge “spontaneously” during virus replication
- ❖ HIV and HBV mutants exist as rare species prior to therapy
- ❖ HCV single/double mutants are often dominant in naïve patients (NS3 and NS5A)
- ❖ Virus replication under drug pressure drives expansion of the mutants – *Natural evolution* → *increasing resistance & fitness*
- ❖ If therapy is stopped, drug susceptible virus tends to outgrow resistant mutants selected by therapy – *mutants persist as enriched minority species*
- ❖ Mutants are archived in HIV DNA provirus and HBV cccDNA

Your turn 😊

Which of the following correctly describes HIV?

- 1. RNA virus, high replication during AIDS phase only**
- 2. RNA virus, high replication, stable genetic make-up**
- 3. RNA virus, high replication, rapid genetic evolution**

Your turn 😊

Which of the following correctly describes HIV?

- 1. RNA virus, high replication during AIDS phase only**
- 2. RNA virus, high replication, stable genetic make-up**
- 3. RNA virus, high replication, rapid genetic evolution**

Your turn 😊

Which of the following correctly describes HBV?

- 1. HBV polymerase lacks reverse transcriptase activity**
- 2. The genomic structure favours rapid emergence of resistance**
- 3. Resistance is less of a problem with 3rd gen drugs**

Your turn 😊

Which of the following correctly describes HBV?

- 1. HBV polymerase lacks reverse transcriptase activity**
- 2. The genomic structure favours rapid emergence of resistance**
- 3. Resistance is less of a problem with 3rd gen drugs**

Your turn 😊

Which of the following correctly describes HCV?

- 1. Resistance is created by suboptimal therapy**
- 2. Resistance is selected by suboptimal therapy**
- 3. Resistance is archived in the nucleus of hepatocytes**

Your turn 😊

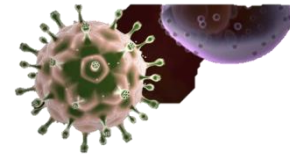
Which of the following correctly describes HCV?

- 1. Resistance is created by suboptimal therapy**
- 2. Resistance is selected by suboptimal therapy**
- 3. Resistance is archived in the nucleus of hepatocytes**

**Well
done!**



The HIV virology timeline



HIV-1 isolated

**HIV-1 genome
sequenced**

**HIV replicates
at high levels
throughout
the infection**

**HIV
replication
drives immune
compromise**

**Highly active
antiretroviral therapy**

**Plasma HIV RNA
(‘viral load’) suppression
as goal of therapy**

**HIV replication
causes disease
through immune
activation &
inflammation**

**HIV
eradication
research**

1982

1985

1991

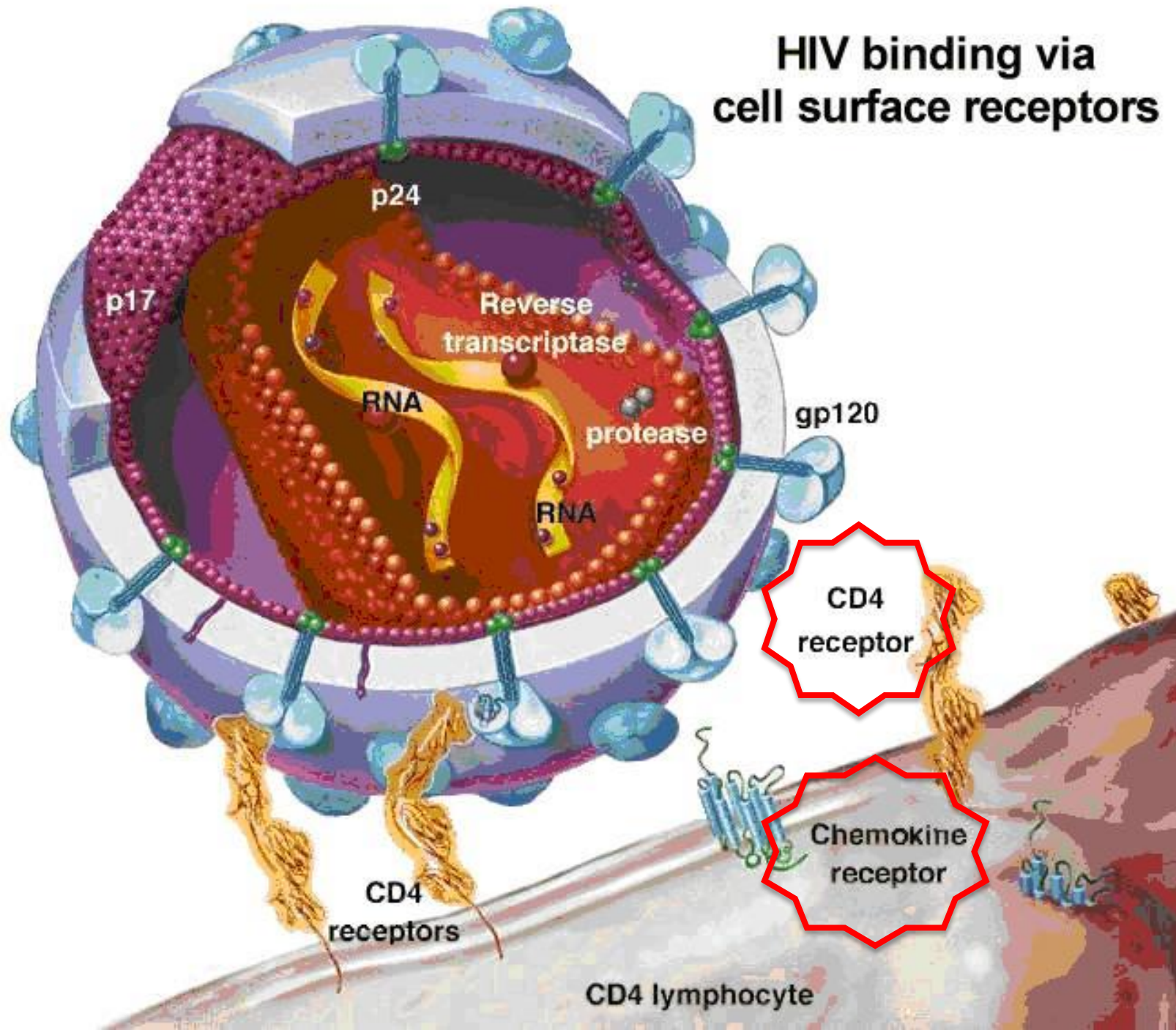
1995

1996

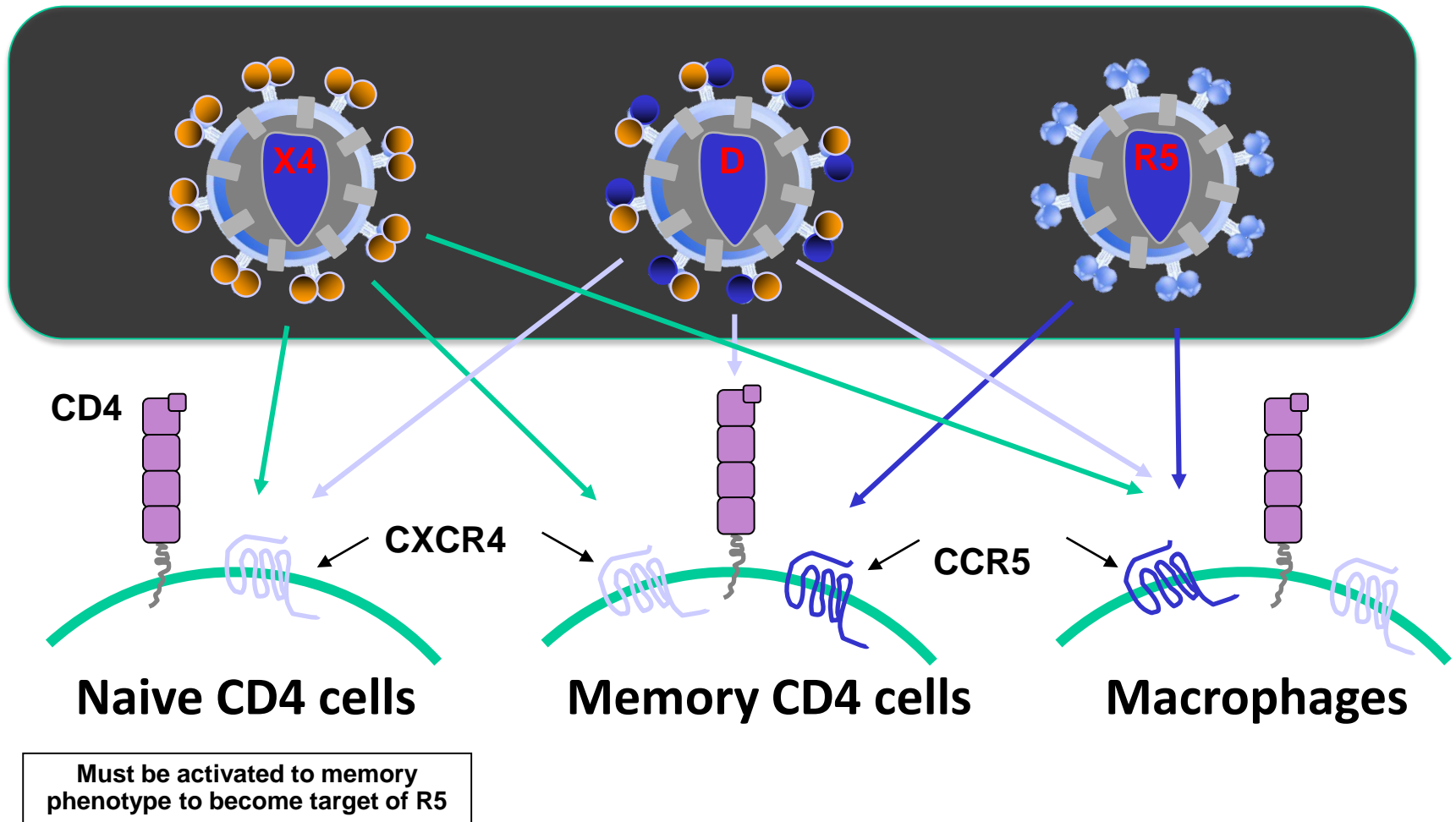
2009

2010 →

HIV binding via cell surface receptors

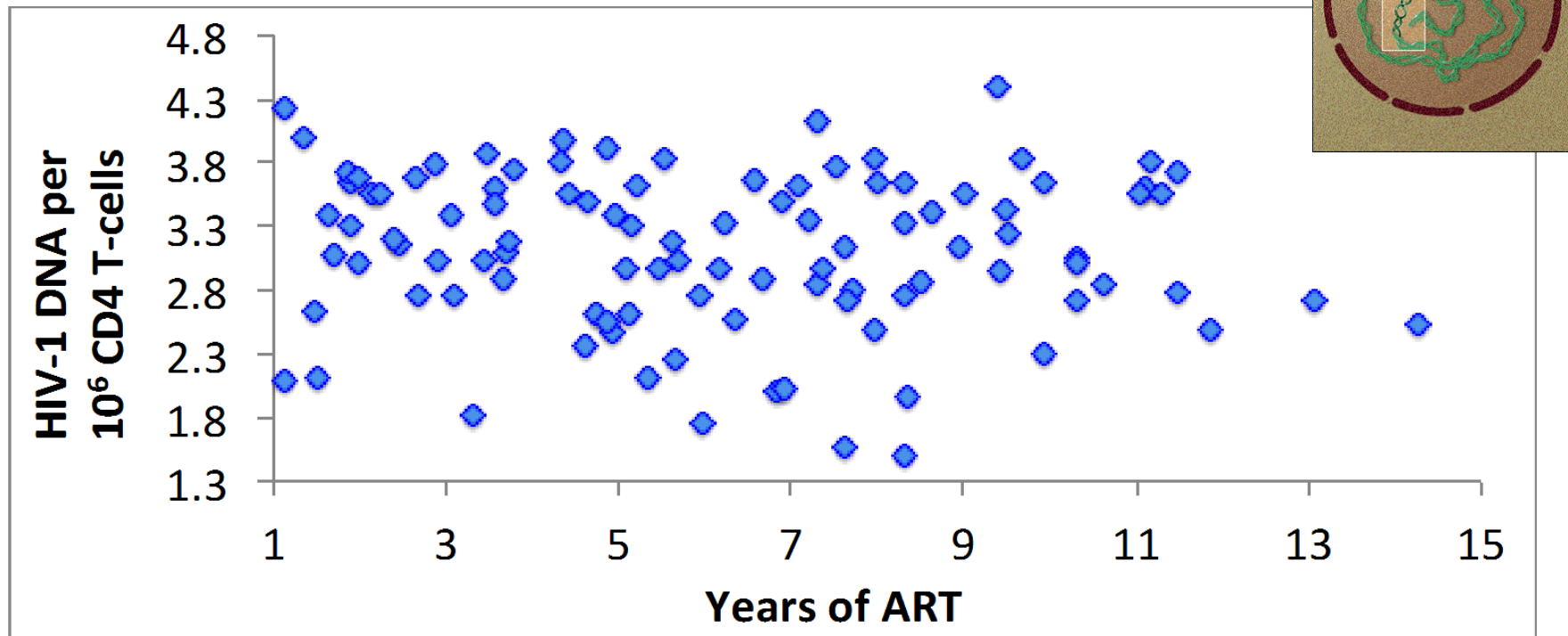


HIV tropism defined by co-receptor use



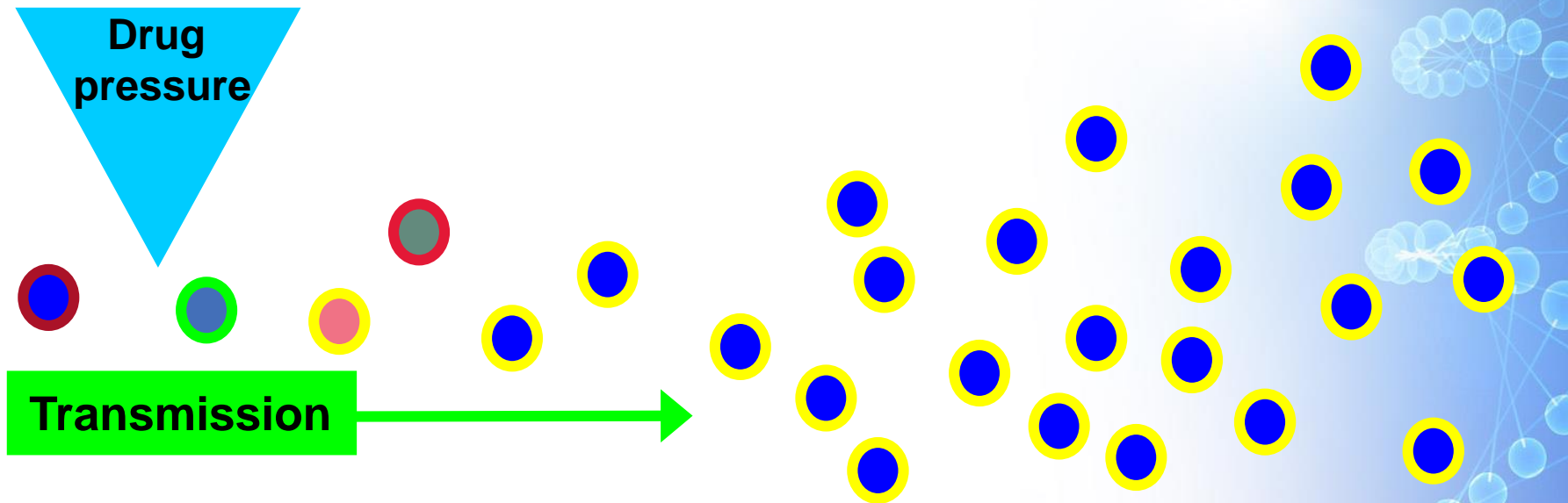
HIV DNA load during antiretroviral therapy

❖ HIV DNA quantified in PBMC



Genetic barrier and cross-resistance

Class	ARVs	Genetic Barrier	Cross Resistance
NRTIs	ZDV/3TC, d4T/3TC	+ / ++	+++
	ABC/3TC, TDF/3TC	+	+++
	TDF/FTC	+ / ++	+++
NNRTIs	EFV, NVP, RPV	+	+++
	ETR	+ / ++	++(+)
PIs	Unboosted	+ / ++	++ / +++
	Boosted	+++ / +++++	+ / ++
Fusion inhibitors	T20	+	NA
CCR5 antagonists	MVC	+ / ++	NA
Integrase inhibitors	RAL, EVG	+	+++
	DTG	++ / ++(+)	++(+)



Transmitted Drug Resistance

Relatively stable after transmission

Gradual reversion over time

Persistence at low frequency in plasma

Persistence in latently infected cells